



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 158815

TO: James Ketter
Location: REM/2A71/2C70
Art Unit: 1636
Friday, July 15, 2005
Case Serial Number: 10/804120

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Ketter,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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OM nucleic - nucleic search, using SW model

Run on: July 13, 2005, 17:30:50 ; Search time 82.6156 Seconds
(without alignments)
6003.565 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79
Sequence: 1 gtcagtttttcgcggggtc.....ctatgacacaggttcaaca 79

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	79	100.0	79	9	US-09-810-521-5
2	79	100.0	79	9	US-09-801-321A-5
3	79	100.0	79	16	US-10-337-985-5
4	79	100.0	79	21	US-10-804-120-5
5	77.4	98.0	79	9	US-09-810-521-4
6	77.4	98.0	79	9	US-09-801-321A-4
7	77.4	98.0	79	16	US-10-337-985-4

8	77.4	98.0	79	21	US-10-804-120-4	Sequence 4, Appli
9	77.4	98.0	1026	10	US-09-746-660A-53	Sequence 53, Appli
10	77.4	98.0	1411	8	US-08-952-976-14	Sequence 14, Appli
11	77.4	98.0	1411	14	US-10-226-136-14	Sequence 14, Appli
12	77.4	98.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
13	61.6	78.0	80	9	US-09-810-521-6	Sequence 6, Appli
14	61.6	78.0	80	9	US-09-801-321A-6	Sequence 6, Appli
15	61.6	78.0	80	16	US-10-337-985-6	Sequence 6, Appli
16	61.6	78.0	80	21	US-10-804-120-6	Sequence 6, Appli
17	40	50.6	40	9	US-09-810-521-16	Sequence 16, Appli
18	40	50.6	40	9	US-09-801-321A-14	Sequence 14, Appli
19	40	50.6	40	16	US-10-337-985-14	Sequence 14, Appli
20	40	50.6	40	21	US-10-804-120-14	Sequence 14, Appli
21	33.6	42.5	40	9	US-09-810-521-18	Sequence 18, Appli
22	33.6	42.5	40	9	US-09-801-321A-16	Sequence 16, Appli
23	33.6	42.5	40	16	US-10-337-985-16	Sequence 16, Appli
24	33.6	42.5	40	21	US-10-804-120-16	Sequence 16, Appli
25	32.6	41.3	39	9	US-09-810-521-17	Sequence 17, Appli
26	32.6	41.3	39	9	US-09-801-321A-15	Sequence 15, Appli
27	32.6	41.3	39	16	US-10-337-985-15	Sequence 15, Appli
28	32.6	41.3	39	21	US-10-804-120-15	Sequence 25, Appli
29	28.4	35.9	30	14	US-10-067-974-25	Sequence 13, App
30	28.2	35.7	47115	18	US-10-052-482-133	Sequence 9671, A
31	28	35.4	742	13	US-10-027-632-99671	Sequence 9672, A
32	28	35.4	742	13	US-10-027-632-99671	Sequence 9672, A
33	28	35.4	742	17	US-10-027-632-99671	Sequence 9672, A
34	28	35.4	742	17	US-10-027-632-99672	Sequence 260979, A
35	27.6	34.9	677	13	US-10-027-632-260979	Sequence 260979, A
36	27.6	34.9	677	17	US-10-027-632-260979	Sequence 61115, A
37	27.6	34.7	320	20	US-10-357-930-61115	Sequence 13, Appli
38	27.2	34.4	36	9	US-09-810-521-15	Sequence 13, Appli
39	27.2	34.4	36	9	US-09-801-321A-13	Sequence 13, Appli
40	27.2	34.4	36	16	US-10-337-985-13	Sequence 13, Appli
41	27.2	34.4	36	21	US-10-804-120-13	Sequence 25059, A
42	26.8	33.9	1007	13	US-10-027-632-252059	Sequence 25059, A
43	26.8	33.9	1007	17	US-10-027-632-252059	Sequence 2419, Ap
44	26.6	33.7	1071	18	US-10-335-977-2419	Sequence 2420, Ap
45	26.6	33.7	1248	18	US-10-335-977-2420	

ALIGNMENTS

RESULT 1
US-09-810-521-5
Sequence 5, Appli
Patent No. US20020055153A1
GENERAL INFORMATION:
APPLICANT: KREUTZER, CAROLINE
APPLICANT: MOCKEL, BETTINA
APPLICANT: PEEPERLE, WALTER
APPLICANT: EGGELING, LOTMAR
APPLICANT: SAHM, HERMANN
APPLICANT: PATER, MIROSLAV
TITLE OF INVENTION: L-LYSINE PRODUCING CORYNEBACTERIA AND
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF LYSINE
FILE REFERENCE: 21123/278416/MAS
CURRENT APPLICATION NUMBER: US/09/810,521
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: DE 199 3114.8
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 79
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Data Promoter of C. glutamicum with the
NAME/KEY: mutation
LOCATION: (45)

US-09-810-521-5

Query Match 100.0%; Score 79; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 2

US-09-801-321A-5
; Sequence 5, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:

; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Salm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801.321A
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
; US-09-801-321A-5

Query Match 100.0%; Score 79; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 3

US-10-337-985-5
; Sequence 5, Application US/10337985
; Publication No. US20030162269A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Salm, Hermann
; APPLICANT: Patek, Miroslav

; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
; US-10-337-985-5

Query Match 100.0%; Score 79; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 4

US-10-804-120-5
; Sequence 5, Application US/10804120
; Publication No. US20050074791A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Salm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/804,120
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/10/337,985
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
; US-10-804-120-5

Query Match 100.0%; Score 79; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 5

US-09-810-521-4
; Sequence 4, Application US/09810521
; Patent No. US20020055153A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE PRODUCING CORYNEBACTERIA AND
; FILE REFERENCE: 21123/278416/MAS
; CURRENT APPLICATION NUMBER: US/09/810,521
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: DE 199 31314.8
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: dapa wild-type promoter
US-09-810-521-4

Query Match 98.0%; Score 77.4; DB 9; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 6

US-09-801-321A-4
; Sequence 4, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE-PRODUCING CORYNEBACTERIUM AND PROCESS FOR THE PREPARATION
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801,321A
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
US-09-801-321A-4

Query Match 98.0%; Score 77.4; DB 9; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 7

US-10-337-985-4
; Sequence 4, Application US/10337985
; Publication No. US20030162269A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE-PRODUCING CORYNEBACTERIUM AND PROCESS FOR THE PREPARATION
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
US-10-337-985-4

Query Match 98.0%; Score 77.4; DB 16; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 8

US-10-804-120-4
; Sequence 4, Application US/10804120
; Publication No. US20050074791A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTHAR

APPLICANT: Sahn, Hermann
APPLICANT: Patek, Miroslav
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/804,120
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US/10/337,985
PRIOR FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 79
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(79)
OTHER INFORMATION: dapa wild type promoter
US-10-804-120-4

Query Match 98.0%; Score 77.4; DB 21; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 9
US-09-746-660A-53
Sequence 53, Application US/09746660A
Publication No. US20030049804A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121C22
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 53
LENGTH: 1026
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:

NAME/KEY: CDS
LOCATION: (101)..(1003)
OTHER INFORMATION: RXA00865
US-09-746-660A-53

Query Match 98.0%; Score 77.4; DB 10; Length 1026;
Best Local Similarity 98.7%; Pred. No. 4.8e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Db 40 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99
Qy 61 TATGACACAGGTTTAA 79
Db 100 TATGACACAGGTTTAA 118

RESULT 10
US-08-952-976-14

Sequence 14, Application US/08952976
Publication No. US20020086370A1
GENERAL INFORMATION:

APPLICANT: OTSUNA, Seiko
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: IZUI, Masako
APPLICANT: HAYAKAWA, Atsushi
APPLICANT: NAKANO, Eiichi
APPLICANT: KOBAYASHI, Masaki
APPLICANT: YOSHIMURA, Yasuhiko
APPLICANT: NAKAMATSU, Tsuyoshi
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
CORRESPONDENCE ADDRESSES: 24
NUMBER OF SEQUENCES: 24
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-140614
FILING DATE: 07-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-952-976-14

Query Match 98.0%; Score 77.4; DB 8; Length 1411;
Best Local Similarity 98.7%; Pred. No. 5.2e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 60
DB 250 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 309
QY 61 TATGACACAGGTTTAA 79
DB 310 TATGACACAGGTTTAA 328

RESULT 11
US-10-226-136-14

Sequence 14, Application US/10226136
Publication No. US2003054506A1
GENERAL INFORMATION:
APPLICANT: OTSUNA, Seiko
SUGIMOTO, Masakazu
IZUI, Masako
HAYAKAWA, Atsuehi
NAKANO, Eiichi
KOBAYASHI, Masaki
YOSHIMURA, Yasuhiko
NAKAMATSU, Tsuyoshi

TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,136
FILING DATE: 23-Aug-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: JP 7-140614
FILING DATE: 07-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869

FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-226-136-14

Query Match 98.0%; Score 77.4; DB 14; Length 1411;
Best Local Similarity 98.7%; Pred. No. 5.2e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 60
DB 250 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 309
QY 61 TATGACACAGGTTTAA 79
DB 310 TATGACACAGGTTTAA 328

RESULT 12
US-09-738-626-1/c

Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/37484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

US-09-738-626-1
Query Match 98.0%; Score 77.4; DB 9; Length 3309400;
Best Local Similarity 98.7%; Pred. No. 4.7e-17;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 60
DB 2080244 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAAGATGTAACTTGAATC 2080185
QY 61 TATGACACAGGTTTAA 79
DB 2080184 TATGACACAGGTTTAA 2080166

RESULT 13
US-09-810-521-6

Sequence 6, Application US/09810521
Patent No. US20020055153A1
GENERAL INFORMATION:
APPLICANT: KREUTZER, CAROLINE
APPLICANT: MOCKEL, BETTINA
APPLICANT: PFEFFERLE, WALTER
APPLICANT: EGGELE, LOTHAR
APPLICANT: SAHM, HERMANN
APPLICANT: PATEK, MIROSLAV

TITLE OF INVENTION: L-LYSINE PRODUCING CORNEBACTERIA AND
PROCESS FOR THE PREPARATION OF LYSINE
FILE REFERENCE: 21123/278416/MAS

```

; CURRENT APPLICATION NUMBER: US/09/810,521
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: DE 199 31314.8
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: dapa promoter of C. glutamicum with the
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-09-810-521-6

Query Match          78.0%; Score 61.6; DB 9; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAGATGTTAAGTTGAAGT 59
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Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATAGAGGAGATGTTAATTGAAGT 60
    |||||||

QY 60 CTATGACACAGGTTTAAACA 79
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Db 61 CTATGACACAGGTTTAAACA 80
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RESULT 14
US-09-801-321A-6
; Sequence 6, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzler, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801,321A
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(80)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MA16 mutation
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-09-801-321A-6

Query Match          78.0%; Score 61.6; DB 9; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAGATGTTAAGTTGAAGT 59
    |||||||
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATAGAGGAGATGTTAATTGAAGT 60
    |||||||

QY 60 CTATGACACAGGTTTAAACA 79
    |||||||
Db 61 CTATGACACAGGTTTAAACA 80
    |||||||

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Job time : 86.6156 secs

; US-10-337-985-6
; Sequence 6, Application US/10337985
; Publication No. US20030162259A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzler, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(80)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MA16 mutation
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-10-337-985-6

Query Match          78.0%; Score 61.6; DB 16; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAGATGTTAAGTTGAAGT 59
    |||||||
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATAGAGGAGATGTTAATTGAAGT 60
    |||||||

QY 60 CTATGACACAGGTTTAAACA 79
    |||||||
Db 61 CTATGACACAGGTTTAAACA 80
    |||||||
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 17:08:30 ; Search time 19.2529 Seconds
(without alignments)
6714.112 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79

Sequence: 1 gtagagtttttgcgggggtt.....ctatgacacagtttaca 79

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*

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5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfile1.seq:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	79	3 US-09-353-133-5	Sequence 5, Appl1
2	79	100.0	79	4 US-10-337-985-5	Sequence 5, Appl1
3	77.4	98.0	79	3 US-09-353-133-4	Sequence 4, Appl1
4	77.4	98.0	79	4 US-10-337-985-4	Sequence 4, Appl1
5	77.4	98.0	1411	1 US-08-674-168-18	Sequence 18, Appl1
6	77.4	98.0	1411	3 US-08-885-908-14	Sequence 14, Appl1
7	77.4	98.0	1411	3 US-08-852-730-19	Sequence 19, Appl1
8	61.6	78.0	80	3 US-09-353-133-6	Sequence 6, Appl1
9	61.6	78.0	80	4 US-10-337-985-6	Sequence 6, Appl1
10	40	50.6	40	4 US-10-337-985-14	Sequence 14, Appl1
11	33.6	42.5	40	4 US-10-337-985-16	Sequence 16, Appl1
12	32.6	41.3	39	4 US-10-337-985-15	Sequence 15, Appl1
13	32.6	41.3	36	4 US-10-337-985-13	Sequence 13, Appl1
14	26.4	33.4	601	4 US-09-949-001-402	Sequence 402, App
15	26.4	33.4	312957	4 US-09-949-001-31	Sequence 31, Appl1
16	26.4	33.4	312972	4 US-09-949-001-34	Sequence 34, Appl1
17	26.2	33.2	601	4 US-09-949-016-138753	Sequence 138753, A
18	25.8	32.7	32958	4 US-09-949-016-15677	Sequence 15677, A
19	25.8	32.7	36317	4 US-09-949-016-12697	Sequence 12697, A
20	25.8	32.7	36332	4 US-09-949-016-14047	Sequence 14047, A
21	25	31.6	601	4 US-09-949-016-138754	Sequence 138754, A
22	25	31.6	1431	1 US-08-451-715A-11	Sequence 11, Appl1
23	25	31.6	194889	4 US-09-949-016-15654	Sequence 15654, A
24	24.6	31.1	601	4 US-09-949-016-46647	Sequence 46647, A
25	24.6	31.1	14761	4 US-09-949-016-14181	Sequence 14181, A
26	24.6	31.1	14823	4 US-09-949-016-12124	Sequence 12124, A
27	24.6	31.1	89689	4 US-09-949-016-13089	Sequence 13089, A

C	28	24.4	30.9	601	4	US-09-949-016-45241	Sequence 45241, A
	29	24.4	30.9	18888	4	US-09-949-016-16386	Sequence 16386, A
	30	24.4	30.9	27223	4	US-09-949-016-11036	Sequence 11036, A
	31	24.2	30.6	601	4	US-09-949-016-113337	Sequence 113337, A
	32	24.2	30.6	705	4	US-09-107-532A-1629	Sequence 1629, Ap
	33	24.2	30.6	2142	4	US-09-949-016-4818	Sequence 4818, Ap
	34	24.2	30.6	2474	4	US-09-774-528-137	Sequence 137, App
	35	24.2	30.6	21045	4	US-09-949-016-16560	Sequence 16560, A
	36	24.2	30.6	155266	4	US-09-949-016-113870	Sequence 113870, A
	37	24.2	30.6	285986	4	US-09-949-016-13287	Sequence 13287, A
	38	24.2	30.6	288031	4	US-09-949-016-14864	Sequence 14864, A
	39	23.8	30.1	365	4	US-09-270-767-6267	Sequence 6267, Ap
	40	23.8	30.1	365	4	US-09-270-767-21549	Sequence 21549, A
	41	23.8	30.1	15817	4	US-09-949-016-16496	Sequence 16496, A
	42	23.6	29.9	654	3	US-08-936-165A-234	Sequence 234, App
	43	23.6	29.9	936	3	US-08-910-501-3	Sequence 3, Appl1
	44	23.6	29.9	936	3	US-09-398-550-3	Sequence 3, Appl1
	45	23.6	29.9	939	3	US-08-910-501-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-353-133-5
; Sequence 5, Application US/09353133
; Patent No. 6200785
; GENERAL INFORMATION:
; APPLICANT: Degussa-Höls AG
; TITLE OF INVENTION: Forschungszentrum Jülich GmbH
; TITLE OF INVENTION: L-lysine-producing Corynebacteria and process for the
; FILE REFERENCE: 990058 BT
; CURRENT APPLICATION NUMBER: US/09/353,133
; CURRENT FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Synthetic sequence
; FEATURE:
; OTHER INFORMATION: Description of the synthetic sequence:
; OTHER INFORMATION: dapa promoter of C. glutamicum with the
; OTHER INFORMATION: MC20-Mutation
; NAME/KEY: mutation
; LOCATION: (45)
; US-09-353-133-5

Query Match          100.0%; Score 79; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTCGCGGGTGTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTCGCGGGTGTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 60
DB 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 2
US-10-337-985-5
; Sequence 5, Application US/10337985
; Patent No. 6746855
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter

```

```
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Mirosław
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; TITLE OF INVENTION: of L-Lysine
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MC20 mutation
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (45)
; US-10-337-985-5
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Query Match          100.0%; Score 79; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
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QY 61 TATGACACACAGGTTTAA 79
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DB 61 TATGACACACAGGTTTAA 79
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RESULT 3
US-09-353-133-4
; Sequence 4, Application US/09353133
; Patent No. 6200785
; GENERAL INFORMATION:
; APPLICANT: Degussa-Höls AG
; TITLE OF INVENTION: L-Lysine-producing corynebacteria and process for the
; FILE REFERENCE: 990058 BT
; CURRENT APPLICATION NUMBER: US/09/353,133
; CURRENT FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: dapa wild-type promoter
; US-09-353-133-4
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Query Match          98.0%; Score 77.4; DB 3; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.8e-21;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
    |||||||
QY 61 TATGACACACAGGTTTAA 79
    |||||||
DB 61 TATGACACACAGGTTTAA 79
    |||||||
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RESULT 4
US-10-337-985-4
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; Sequence 4, Application US/10337985
; Patent No. 6746855
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
; US-10-337-985-4
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Query Match          98.0%; Score 77.4; DB 4; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.8e-21;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
    |||||||
QY 61 TATGACACACAGGTTTAA 79
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DB 61 TATGACACACAGGTTTAA 79
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RESULT 5
US-08-674-168-18
; Sequence 18, Application US/08674168
; Patent No. 5804414
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Mika
; APPLICANT: MATSUI, Hiroshi
; APPLICANT: YOKOZAKI, Kenzo
; APPLICANT: HIRANO, Seiko
; APPLICANT: HAYAKAWA, Atsushi
; APPLICANT: IZUI, Masako
; APPLICANT: SUGIMOTO, Masakazu
; TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
; TITLE OF INVENTION: ARTIFICIAL TRANSPROSON
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,168
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-674-168-18

Query Match 98.0%; Score 77.4; DB 1; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1.5e-20;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 60
Db 250 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 309

Qy 61 TATGAGCACAGGTTTAA 79
Db 310 TATGAGCACAGGTTTAA 328

RESULT 6
US-08-985-908-14
Sequence 14, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIMURA, AND TSUYOSHI NA
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 1411 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-985-908-14

Query Match 98.0%; Score 77.4; DB 3; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1.5e-20;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 60
Db 250 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAATC 309

Qy 61 TATGAGCACAGGTTTAA 79
Db 310 TATGAGCACAGGTTTAA 328

RESULT 7
US-08-852-730-19
Sequence 19, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS

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LOCATION: 311..1213
US-08-852-730-19
Query Match
Best Local Similarity 98.0%; Score 77.4; DB 3; Length 1411;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Db 250 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 309

Qy 61 TATGAGCACAGGTTTAA 79
Db 310 TATGAGCACAGGTTTAA 328

RESULT 8
US-09-353-133-6
Sequence 6, Application US/09353133
Patent No. 6200785
GENERAL INFORMATION:
APPLICANT: Degussa-Hols AG
TITLE OF INVENTION: L-Lysine-producing corynebacteria and process for the
FILE REFERENCE: 990058 BT
CURRENT APPLICATION NUMBER: US/09/353,133
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 80
TYPE: DNA
ORGANISM: Synthetic sequence
FEATURE:
OTHER INFORMATION: Description of the synthetic sequence:
OTHER INFORMATION: dapA promoter of C. glutamicum with the
FEATURE:
NAME/KEY: mutation
LOCATION: (35)..(53)
US-09-353-133-6

Query Match
Best Local Similarity 78.0%; Score 61.6; DB 3; Length 80;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAAT 59
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAATTTGAAT 60

Qy 60 CTATGAGCACAGGTTTAA 79
Db 61 CTATGAGCACAGGTTTAA 80

RESULT 9
US-10-337-985-6
Sequence 6, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzler, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
APPLICANT: Patek, Miroslav
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
FILE REFERENCE: 21123/278409
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
```

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CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(80)
OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MA16 mutation
FEATURE:
NAME/KEY: mutation
LOCATION: (35)..(53)
US-10-337-985-6

Query Match
Best Local Similarity 78.0%; Score 61.6; DB 4; Length 80;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAAT 59
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAATTTGAAT 60

Qy 60 CTATGAGCACAGGTTTAA 79
Db 61 CTATGAGCACAGGTTTAA 80

RESULT 10
US-10-337-985-14/C
Sequence 14, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzler, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
APPLICANT: Patek, Miroslav
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(40)
OTHER INFORMATION: PCR primer
US-10-337-985-14

Query Match
Best Local Similarity 50.6%; Score 40; DB 4; Length 40;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 CCAATGAGGAGATGTAACCTTGAATCTATGAGCAC 69
Db 40 CCAATGAGGAGATGTAACCTTGAATCTATGAGCAC 1

RESULT 11
US-10-337-985-16/C
Sequence 16, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
```

APPLICANT: Kreutzer, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahn, Hermann
APPLICANT: Patek, Mirosław
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(40)
OTHER INFORMATION: PCR primer
US-10-337-985-16

Query Match 42.5%; Score 33.6; DB 4; Length 40;
Best Local Similarity 90.0%; Pred. No. 0.00079;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 30 CCAATGAGGGAAGATGTTAAGCTTGAAGCTTATGAGCAG 69
Db 40 CCAATGAGGGAAGATGTTAAGCTTGAAGCTTATGAGCAG 1

RESULT 12
US-10-337-985-15
Sequence 15, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzer, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahn, Hermann
APPLICANT: Patek, Mirosław
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(39)
OTHER INFORMATION: PCR primer
US-10-337-985-15

Query Match 41.3%; Score 32.6; DB 4; Length 39;
Best Local Similarity 89.7%; Pred. No. 0.0019;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 30 CCAATGAGGGAAGATGTTAAGCTTGAAGCTTATGAGCAG 68
Db 1 CCAATGAGGGAAGATGTTAAGCTTGAAGCTTATGAGCAG 39

RESULT 13
US-10-337-985-13
Sequence 13, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzer, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahn, Hermann
APPLICANT: Patek, Mirosław
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(36)
OTHER INFORMATION: PCR primer
US-10-337-985-13

Query Match 34.4%; Score 27.2; DB 4; Length 36;
Best Local Similarity 90.6%; Pred. No. 0.26;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 37 AGGGAAGATGTTAAGCTTGAAGCTTATGAGCAG 68
Db 5 ATGAGAGATGTTAAGCTTGAAGCTTATGAGCAG 36

RESULT 14
US-09-949-001-402
Sequence 402, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 402
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-001-402

Query Match 33.4%; Score 26.4; DB 4; Length 601;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 17 GGTGTTTAAACCCCAATGAGGGAAGATGTTAAGCTTGAAGCTC 60
Db 24 GTTGTAAACCTTCAAGAGGGAAGATGTTGCTTGAATTC 67

RESULT 15
US-09-949-001-31
Sequence 31, Application US/09949001
Patent No. 6825336

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 312957
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(312957)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-001-31
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Query_Match 33.4%; Score 26.4; DB 4; Length 312957;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 17 GATTGTTTACCCCAATGAGGAGAGATGTAACCTTGAACTC 60
DB 129890 GATTGTTTAAACCTTTCAGAGAGAGAGAGGTTGCCCTTGAAATTC 129933
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Search completed: July 13, 2005, 19:44:56
Job time : 21.2529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 16:24:26 ; Search time 372.764 Seconds
(without alignments)
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Title: US-10-804-120-5

Sequence: 1 gtagagtttttcgcgggggtt.....ctatgagcacagtttaca 79

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: gb_ba:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	79	6	AR138936 Sequence
2	79	100.0	79	6	AR544598 Sequence
3	79	100.0	79	6	AX137605 Sequence
4	79	100.0	79	6	AX137726 Sequence
5	79	100.0	79	6	BD006805 L-tycin-P
6	79	100.0	79	6	BD010850 Coryneb
7	77.4	98.0	79	6	AR138935 Sequence
8	77.4	98.0	79	6	AR544597 Sequence
9	77.4	98.0	79	6	AX137604 Sequence
10	77.4	98.0	79	6	AX137725 Sequence
11	77.4	98.0	79	6	BD006804 L-tycin-P
12	77.4	98.0	79	6	BD010849 Coryneb
13	77.4	98.0	1026	6	AX063773 Sequence
14	77.4	98.0	1026	6	AX244061 Sequence
15	77.4	98.0	1341	1	CGDAPAG
16	77.4	98.0	1341	1	CGDAPAG
17	77.4	98.0	1411	6	AR038113 Sequence
18	77.4	98.0	1411	6	AR095435 Sequence
19	77.4	98.0	1411	6	E12767 DNA encodin

20	77.4	98.0	1411	6	E14517	E14517 DNA encodin
21	77.4	98.0	1411	6	E16752	E16752 gDNA encodi
22	77.4	98.0	1902	1	CGDAPB	X67737 C.Glutamicu
23	77.4	98.0	3572	1	BLDAPB	Z21502 B.lactoferm
24	77.4	98.0	337200	1	AP005280	AP005280 Coryneb
25	77.4	98.0	349584	1	BP272153	BP272153 Coryneb
26	77.4	98.0	349980	6	AX127149	AX127149 Sequence
27	77.4	98.0	78.0	80	AR138937	AR138937 Sequence
28	61.6	78.0	80	6	AR544599	AR544599 Sequence
29	61.6	78.0	80	6	AX137606	AX137606 Sequence
30	61.6	78.0	80	6	AX137727	AX137727 Sequence
31	61.6	78.0	80	6	BD006806	BD006806 L-tycin-P
32	61.6	78.0	80	6	BD010851	BD010851 Coryneb
33	48.2	61.0	1333	6	E54479	E54479 Heat-resist
34	48.2	61.0	3063	1	AB083130	AB083130 Coryneb
35	48.2	61.0	303250	1	AP005220	AP005220 Coryneb
36	40	50.6	40	6	AR544607	AR544607 Sequence
37	33.6	42.5	40	6	AR544609	AR544609 Sequence
38	32.6	41.3	39	6	AR544608	AR544608 Sequence
39	30.4	38.5	165921	9	AC009159	AC009159 Homo sapi
40	29.8	37.7	234797	2	AC130921	AC130921 Rattus no
41	29.8	37.7	254796	2	AC097920	AC097920 Rattus no
42	29.6	37.5	213462	10	AC077689	AC077689 Mus Muscu
43	29.6	37.5	219769	10	AC067964	AC067964 Mus Muscu
44	29.4	37.2	148937	2	AC015902	AC015902 Homo sapi
45	29.4	37.2	205000	2	CR533575	CR533575 Danio rer

ALIGNMENTS

RESULT 1	AR138936	Sequence 5 from patent US 6200785.	79 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR138936					
DEFINITION	Sequence 5 from patent US 6200785.					
ACCESSION	AR138936					
VERSION	AR138936.1	GI:14481281				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 79)					
AUTHORS	Kreutzer, C., Hans, S., Rieping, M., Mockel, B., Pfeiffer, W., Eggeling, L., Sahm, H. and Patek, M.					
TITLE	L-lysine-producing corynebacteria and process for the preparation of L-lysine					
JOURNAL	Patent: US 6200785-A 5 13-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..79					
ORIGIN	/organism="unknown"					
	/mol_type="unassigned DNA"					

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Best Local Similarity	100.0%	Pred. No. 6.4e-17;		
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Gaps	0;			
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DB	1	GTTAGGTTTTTTCGCGGGTGTGTTTAAACCCCAATGAGGAAAGATGTAACCTTGAACTC	60	
QY	61	TATGACACAGGTTTAAACA 79		
DB	61	TATGACACAGGTTTAAACA 79		
LOCUS	AR544598			
DEFINITION	Sequence 5 from patent US 6746855.			
ACCESSION	AR544598			
VERSION	AR544598.1	GI:53937424		
KEYWORDS				

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreutzer,C., Hans,S., Rieping,M., Mockel,B., Pfefferle,W., Eggeling,L., Sahn,H. and Patek,M.
TITLE L-lysine-producing corynebacteria and process for the preparation of L-lysine
JOURNAL Patent: US 674685-A 5 08-JUN-2004;
FEATURES Location/Qualifiers
source 1..79
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60
Db 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60

QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 3
AX137726 79 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 5 from Patent EP1067193.
AX137605
VERSION AX137605.1 GI:14273792
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kreutzer,C., Mockel,B., Pfefferle,W., Eggeling,L., Sahn,H. and Patek,M.
TITLE L-lysine producing coryneform bacteria and methods for the production of L-lysine
JOURNAL Patent: EP 1067193-A 5 10-JAN-2001;
FEATURES Degussa AG (DE) ; Forschungszentrum Juelich (DE)
source Location/Qualifiers
1..79
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="dapA-Promotor von C. glutamicum mit der MC20-Mutation"

ORIGIN
variation 45

Query Match 100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60
Db 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60

QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 4
AX137726 79 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 5 from Patent EP1067192.
AX137726

VERSION AX137726.1 GI:14273900
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mockel,B., Pfefferle,W., Kreutzer,C., Hans,S., Rieping,M., Eggeling,L., Sahn,H. and Patek,M.
TITLE L-lysine producing coryneform bacteria and methods for the production of L-lysine
JOURNAL Patent: EP 1067192-A 5 10-JAN-2001;
FEATURES Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="dapA-Promotor von C. glutamicum mit der MC20-Mutation"

ORIGIN
variation 45

Query Match 100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60
Db 1 GTTAGGTTTTTGGCGGGGTTTAAACCCCAATGAGGAGATGTTAAGTTGAATCTC 60

QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 5
BD006805 79 bp DNA linear PAT 09-JAN-2004
LOCUS L-licin-productible corynebacteria, replicable DNA among them,
process for producing L-licin, and strains of E. coli and Corynebacterium glutamicum.
BD006805
VERSION BD006805.1 GI:18635176
KEYWORDS JP 2001037495-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 79)
AUTHORS Creutzer,C., Meckel,V., Puffeffare,W., Eggeling,L., Zamu,H. and Patek,M.
TITLE L-licin-productible corynebacteria, replicable DNA among them,
process for producing L-licin, and strains of E. coli and Patent: JP 2001037495-A 4 13-FEB-2001;
JOURNAL DEGUSSA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH
FEATURES OS Artificial Sequence
PN JP 2001037495-A/4
PD 13-FEB-2001
PF 04-JUL-2000 JP 2000202550
PI 07-JUL-1999 DE 19931314.8
PC CAROLINE CREUTZER, VETTINA MECKEL, WALTHER PUPEFFARE, PI LOTHAR EGGERING,
PI HERMANN ZAMU, MIROSURAFU PATEKU
PC C12N15/09, C12N1/21, C12P13/08 // (C12N1/21, C12R1:15), (C12N1/21, C12R1:19),
PC (C12P13/08, C12R1:15), C12N15/00
CC
FH Key Location/Qualifiers
FT mutation (45).
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"


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ORIGIN
Query Match      100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
    |||||||
DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGAGCACAGGTTTAA 79
    |||||||
DB 61 TATGAGCACAGGTTTAA 79

RESULT 6
LOCUS BD010850 79 bp DNA linear PAT 31-JAN-2002
DEFINITION Corynebacterium producing L-ricin and process for producing L-ricin.
ACCESSION BD010850
VERSION BD010850.1 GI:18639223
KEYWORDS JP 2001061485-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 79)
AUTHORS Meckel,V., Pfefferle,W., Kreuzer,C., Hane,S., Rieping,M., Eggerling,L., Sahm,H. and Patek,M.
TITLE Corynebacterium producing L-ricin and process for producing L-ricin
JOURNAL Patent: JP 2001061485-A 4 13-MAR-2001;
COMMENT DEGUSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH
OS Artificial Sequence
PN JP 2001061485-A/4
PD 13-MAR-2001 JP 2000202551
PR 04-JUL-2000 JP 2000202551
PF 07-JUL-1999 DE 19931317.2
PI VETTYNA MECKEL,WALTER PFEFFERLE,CAROLINE KREUZER,STEPHEN HANS, PI MECHTHILD RIEPING,LOTHAR EGGERING,HERMANN SAHM, PI MIKROBIAFUF PATEKU
PC C12N15/09,C12N1/21,C12P13/08//C12N15/09,C12R1.15),(C12N1/21,C12R1.15),
PC C12N1/21,C12R1.19),(C12P13/08,C12R1.15),C12N15/00,(C12N15/00,C12R1.15)
CC
FH
FT Key Location/Qualifiers
mutation (45).
1..79 Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
    |||||||
DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGAGCACAGGTTTAA 79
    |||||||
DB 61 TATGAGCACAGGTTTAA 79

RESULT 7
LOCUS AR138935 79 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 4 from patent US 6200785.
ACCESSION AR138935
VERSION AR138935.1 GI:14481280

```

```

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreuzer,C., Hane,S., Rieping,M., Meckel,B., Pfefferle,W., Eggerling,L., Sahm,H. and Patek,M.
TITLE L-lysine-producing corynebacteria and process for the preparation of L-lysine
JOURNAL Patent: US 6200785-A 4 13-MAR-2001;
FEATURES
source Location/Qualifiers
1..79
/mol_type="unassigned DNA"

ORIGIN
Query Match      98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79

RESULT 8
LOCUS AR544597 79 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 4 from patent US 6746855.
ACCESSION AR544597
VERSION AR544597.1 GI:53937423
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreuzer,C., Hane,S., Rieping,M., Meckel,B., Pfefferle,W., Eggerling,L., Sahm,H. and Patek,M.
TITLE L-lysine-producing corynebacteria and process for the preparation of L-lysine
JOURNAL Patent: US 6746855-A 4 08-JUN-2004;
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source Location/Qualifiers
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ORIGIN
Query Match      98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79

RESULT 9
LOCUS AX137604 79 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 4 from patent EP1067193.
ACCESSION AX137604
VERSION AX137604.1 GI:14273791
KEYWORDS Corynebacterium glutamicum
SOURCE Corynebacterium glutamicum

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REFERENCE	Bacteria; Actinobacteriales;
AUTHORS	Kreutzer,C., Moeckel,B., Pfeifferle,W., Eggeling,L., Sahm,H. and Patek,M.
TITLE	L-lysine producing coryneform bacteria and methods for the production of L-lysine
JOURNAL	Patent: EP 1067193-A 4 10-JAN-2001;
DEGUSSE AG (DE) ; FORSCHUNGSZENTRUM JUELICH (DE)	
FEATURES	Location/Qualifiers
SOURCE	1..79 /organism="Corynebacterium glutamicum" /mol_type="unassigned DNA" /db_xref="taxon:1718" /note="dapa Wildtyp-Promotor"
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Query Match	98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity	98.7%; Pred.No.2.4e-16;
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OY	1 GTTAGAGTTTTTGGCGGGGTGTTTAACCCCAATGAGGAAGATGTAACCTTGAACTC 60
Dn	1 GTTAGAGTTTTTGGCGGGGTGTTTAACCCCAATGAGGAAGATGTAACCTTGAACTC 60
OY	61 TATGAGCACAGGTTTACA 79
Dn	61 TATGAGCACAGGTTTACA 79
RESULT 11	
LOCUS	BD006804 79 bp DNA linear PAT 31-JAN-2002
DEFINITION	L-tricin-producible corynebacteria, replicable DNA among them,

ACCESSION	BD006804	1 GI:18635175	Corynebacterium glutamicum.
VERSION	BD006804.1	GI:18635175	
KEYWORDS	JP 2001037495-A/3.		
SOURCE	Corynebacterium glutamicum		
ORGANISM	Corynebacterium glutamicum		
REFERENCE	Bacteria; Actinobacteria; Actinomycetales;		
AUTHORS	Corynebacteriaceae; Corynebacterium.		
TITLE	1 (bases 1 to 79)		
JOURNAL	Creuzer,C., Meckel,V., Pfeiffer,W., Eggering,L., Zamu,H. and Patek,M.		
COMMENT	L-ricin-productible corynebacteria, replicable DNA among them, process for producing L-ricin, and strains of E. coli and Patent: JP 2001037495-A 3 13-FEB-2001.		
	DEUTSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH		
	OS Corynebacterium glutamicum		
	PN JP 2001037495-A/3		
	PD 13-FEB-2001		
	PF 04-JUL-2000 JP 2000202550		
	PR 07-JUL-1999 DE 19931314.8		
	PI CAROLINE CREUZER,VETTYNA MECKEL,WALTHER PUEFFARE, PI LOTMAR EGGERING,		
	PI HERMANN ZAMU,MIROSLAW PATEKU		
	PC C12N15/09,C12N1/21,C12P3/08//C12N1/21,C12R1:15),C12N1/21,		
	PC C12R1:19)		
	PC C12P13/08,C12R1:15),C12N15/00		
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	FH		
	FT Key source Location/Qualifiers		
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Query Match	98.0%; Score 77.4; DB 6; Length 79;		
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Matches	78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY	1 GTTAGGTTTTTGGGGGTGTTTAACCCCAATAGGAGAGTGTAACCTGAAGTC 60		
Dn	1 GTTAGGTTTTTGGGGGTGTTTAACCCCAATAGGAGAGTGTAACCTGAAGTC 60		
OY	61 TATGACACAGGTTTAAACA 79		
Dn	61 TATGACACAGGTTTAAACA 79		
RESULT 12			
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LOCUS	BD010849	79 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Corynebacterium producing L-ricin and process for producing		
ACCESION	BD010849		
VERSION	BD010849.1		
KEYWORDS	GI:18639222		
SOURCE	JP 2001061485-A/3.		
ORGANISM	Corynebacterium glutamicum		
	Corynebacterium glutamicum		
	Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;		
	Corynebacteriaceae; Corynebacterium.		
	1 (bases 1 to 79)		
	Meckel,V., Pfeiffer,W., Kreuzer,C., Hans,S., Rieping,M.,		
	Eggering,L., Sahm,H. and Pateku,M.		
	Corynebacterium producing L-ricin and process for producing L-ricin		
	Patent: JP 2001061485-A 3 13-MAR-2001;		
	DEUTSA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH		
	OS Corynebacterium glutamicum		
	PN JP 2001061485-A/3		
	PD 13-MAR-2001		
	PF 04-JUL-2000 JP 2000202551		

PR 07-JUL-1999 DE 19931317.2
 PI VERTYVA MECKEL, WALTER PEEFERLE, CAROLINE CREUZER, STEPHEN HANS,
 PI MECHTILD RIEPING, IOTHA RIEGERING, HERMANN SAHM, PI
 MIROSLAV PATEK
 PC C12N15/09, C12N1/21, C12P13/08 // (C12N15/09, C12R1:15), (C12N1/21,
 PC C12R1:15),
 PC (C12N1/21, C12R1:19), (C12P13/08, C12R1:15), C12N15/00, (C12N15/00,
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 Query Match 98.0%; Score 77.4; DB 6; Length 79;
 Best Local Similarity 98.7%; Pred. No. 2.4e-16;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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QY 61 TATGACACAGGTTTAA 79
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 DB 61 TATGACACAGGTTTAA 79
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RESULT 13
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 DEFINITION Sequence 55 from Patent WO0100843.
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 AX063773.1 GI:12541485
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 /db_xref="GI:12541485"
 /note="unnamed protein product; RXA00865"

REFERENCE
 AUTHORS Pompejus, M., Kroege, B., Schroeder, H., Zelder, O., and Haberbauer, G.
 TITLE Corynebacterium glutamicum genes encoding metabolic pathway
 JOURNAL BASF AKTIENGESSELLSCHAFT (DE)
 LOCATION/Qualifiers
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FEATURES
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 CDS
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ORIGIN
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 Best Local Similarity 98.7%; Pred. No. 1.9e-16;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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 DB 40 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99
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QY 61 TATGACACAGGTTTAA 79
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 DB 100 TATGACACAGGTTTAA 118
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RESULT 14
 LOCUS AX244061 1026 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 53 from Patent WO0166573.
 AX244061
 AX244061.1 GI:15859125
 /transl_table=1
 /protein_id="C15859125"
 /db_xref="GI:15859125"
 /note="unnamed protein product; RXA00865"

REFERENCE
 AUTHORS Pompejus, M., Kroege, B., Schroeder, H., Zelder, O., Haberbauer, G.,
 Kim, J.W., Lee, H.S. and Hwang, B.J.
 TITLE Corynebacterium glutamicum genes encoding metabolic pathway
 JOURNAL BASF AKTIENGESSELLSCHAFT (DE)
 LOCATION/Qualifiers
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 /organism="Corynebacterium glutamicum"
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 101..1006
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ORIGIN
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 Best Local Similarity 98.7%; Pred. No. 1.9e-16;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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 DB 40 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99
 |||||

QY 61 TATGACACAGGTTTAA 79
 |||||
 DB 100 TATGACACAGGTTTAA 118
 |||||

RESULT 15
 LOCUS AJ584662 1341 bp DNA linear BCT 04-OCT-2003
 DEFINITION Corynebacterium glutamicum dapA gene for dihydrodipicolinate
 synthetase.
 AJ584662
 AJ584662.1 GI:37515386
 /transl_table=1
 /protein_id="C37515386"
 /db_xref="GI:37515386"
 /note="unnamed protein product; RXA00865"

REFERENCE
 AUTHORS Vu Kim, T., Le Van, H., Duong Hong, Q., Nguyen Thuy, C. and Dinh Duy, K.
 TITLE Cloning of the gene coding for dihydrodipicolinate synthetase from

DB 40 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99
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 QY 61 TATGACACAGGTTTAA 79
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 DB 100 TATGACACAGGTTTAA 118
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RESULT 14
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 DEFINITION Sequence 53 from Patent WO0166573.
 AX244061
 AX244061.1 GI:15859125
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 /protein_id="C15859125"
 /db_xref="GI:15859125"
 /note="unnamed protein product; RXA00865"

REFERENCE
 AUTHORS Pompejus, M., Kroege, B., Schroeder, H., Zelder, O., Haberbauer, G.,
 Kim, J.W., Lee, H.S. and Hwang, B.J.
 TITLE Corynebacterium glutamicum genes encoding metabolic pathway
 JOURNAL BASF AKTIENGESSELLSCHAFT (DE)
 LOCATION/Qualifiers
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FEATURES
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 CDS
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ORIGIN
 Query Match 98.0%; Score 77.4; DB 6; Length 1026;
 Best Local Similarity 98.7%; Pred. No. 1.9e-16;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTGCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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QY 61 TATGACACAGGTTTAA 79
 |||||
 DB 100 TATGACACAGGTTTAA 118
 |||||

RESULT 15
 LOCUS AJ584662 1341 bp DNA linear BCT 04-OCT-2003
 DEFINITION Corynebacterium glutamicum dapA gene for dihydrodipicolinate
 synthetase.
 AJ584662
 AJ584662.1 GI:37515386
 /transl_table=1
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 /db_xref="GI:37515386"
 /note="unnamed protein product; RXA00865"

REFERENCE
 AUTHORS Vu Kim, T., Le Van, H., Duong Hong, Q., Nguyen Thuy, C. and Dinh Duy, K.
 TITLE Cloning of the gene coding for dihydrodipicolinate synthetase from

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Corynebacterium glutamicum HN30 isolate
Unpublished
2 (bases 1 to 1341)
Dinh Duy, K.
Direct Submission
Submitted (01-OCT-2003) Dinh Duy K., Molecular Microbiology Lab,
Institute of Biotechnology, NCST, 18, Hoang Quoc Viet, Cau Giay,
Hanoi, 10000, VIET NAM

FEATURES
SOURCE

Location/Qualifiers
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/organism="Corynebacterium glutamicum"
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/db_xref="GI:37515387"

/translation="MSTGLTAKTGVHEHGTGVAMVTPTESGDIDIAGREVAAYLV
DKGIDSLVLAGTGESPTTAAREKLELLKAVREVGDRKLIAGVGNNRTSVELAE
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RRSELPTLIAVKDAGDLVAATSLIKETGLAWYSGDDPLNLVWLALGSSGFISVIGH
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RLPIAMNEQLEALREDMKKAGVL"

ORIGIN

Query Match 98.0%; Score 77.4; DB 1; Length 1341;
Best Local Similarity 98.7%; Pred. No. 1.9e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAAGTC 60
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Db 188 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAAGTC 247
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QY 61 TATGAGCACAGTTTAACA 79
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Db 248 TATGAGCACAGTTTAACA 266
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Job time : 376.764 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 15:18:23 ; Search time 62.0069 Seconds
(without alignments)
7542.061 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	79	100.0	79 4 AAF26024	Aaf26024 C. glutam
3	77.4	98.0	79 4 AAF26006	Aaf26006 C. glutam
4	77.4	98.0	79 4 AAF26023	Aaf26023 C. glutam
5	77.4	98.0	1026 4 AAF21780	Aaf21780 Coryneb
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7	77.4	98.0	1026 4 AAT84782	Aat84782 Brevibac
8	77.4	98.0	1411 2 AAT49281	Aat49281 DNA encod
9	77.4	98.0	1411 2 AAV40256	Aav40256 Brevibac
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11	77.4	98.0	349980 5 AAH65530	Aah65530 C. glutam
12	77.4	98.0	80 4 AAF26008	Aaf26008 C. glutam
13	77.4	98.0	80 4 AAF26025	Aaf26025 C. glutam
14	48.2	61.0	1333 4 AAH45371	Aah45371 C. thermo
15	40	50.6	40 4 AAF26001	Aaf26001 C. glutam
16	40	50.6	40 4 AAF26018	Aaf26018 C. glutam
17	33.6	42.5	40 4 AAF26003	Aaf26003 C. glutam
18	33.6	42.5	40 4 AAF26020	Aaf26020 C. glutam
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20	32.6	41.3	39 4 AAF26019	Aaf26019 C. glutam

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	22	28.2	35.7	47115	9	ADA02627	Ada02627 Mouse Flt
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	24	28.2	35.7	47115	10	ADE95875	Ades95875 Mouse Flt
C	25	27.4	34.7	320	5	ABV61096	Abv61096 Human pro
	26	27.2	34.4	36	4	AAF26000	Aaf26000 C. glutam
	27	27.2	34.4	36	4	AAF26017	Aaf26017 C. glutam
	28	26.6	33.7	2193	13	ADA54856	Ada54856 Bacterial
	29	26.6	33.7	29220	4	AA527653	Aa527653 DNA encod
C	30	26.6	33.7	29220	4	AA527652	Aa527652 DNA encod
	31	26.6	33.7	29220	10	ADB94455	Adb94455 Novel hum
	32	26.6	33.7	29220	10	ADB94456	Adb94456 Novel hum
	33	26.4	33.4	321019	13	ADS36450	Ads36450 Human auto
	34	26.4	33.4	329019	13	ABD32707	Abd32707 Human can
	35	26.2	33.2	609	13	ADO52661	Ado52661 Novel can
	36	32.9	618	8	ACA00742	ACA00742 C. glutam	
	37	32.9	1102	13	ADS17012	AdS17012 B. lichen	
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C	39	26	32.9	349980	5	AAH68531	Aah68531 C. glutam
	40	25.6	32.4	545	6	ABL67098	AbL67098 Thyroid c
	41	25.6	32.4	545	6	ABL68951	AbL68951 Kidney ca
C	42	25.4	32.2	1071	4	ABA88963	AbA88963 Escherich
	43	25.4	32.2	13714	6	ABS79040	AbS79040 E. coli C
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ALIGNMENTS

RESULT 1	AAAF26007	AAAF26007 standard; DNA; 79 BP.
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AC	AAAF26007;	
XX		
DT	20-APR-2001 (first entry)	
XX		
DE	C. glutamicum dapA mutant MC20 promoter DNA fragment SEQ ID 5.	
XX		
KW	lysE, L-lysine; lysine exporter-carrier; dapA; aspartate kinase; lysC;	
KW	dihydropicolinate synthase; pyc; pyruvate carboxylase; dapB; promoter;	
KW	dihydropicolinate reductase; fodor additive; ss.	
XX		
OS	Corynebacterium glutamicum.	
XX		
PN	.EPI067192-Al.	
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PD	10-JAN-2001.	
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PF	06-JUL-2000; 2000BP-00114501.	
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PR	07-JUL-1999; 99DE-01031317.	
XX		
PA	(DEGS) DEGUSSA-HUELS AG.	
XX	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	
PI	Moekkel B, Pfeifferle W, Kreutzer C, Hans S, Rieping M;	
XX	Begging L, Sahn H, Patek M;	
DR	WPI; 2001-125731/14.	
XX		
PT	Coryneform bacteria for high level production of lysine, useful as feed	
PT	additive, overexpresses the lysE and at least one other gene,	
XX	particularly dapA.	
XX		
PS	Claim 4; Page 17; 25pp; German.	
XX		
CC	This invention describes a novel L-lysine producing coryneform bacterium	
CC	(A) with an amplified lysE (lysine exporter-carrier) gene in which at	
CC	least one of the additional genes dapA (dihydropicolinate synthase), lysC	
CC	(aspartate kinase), pyc (pyruvate carboxylase) and/or dapB	
CC	(dihydropicolinate reductase) is amplified and preferably overexpressed.	

CC L-lysine is used as a fodder additive for animals. Overexpression of the
CC additional genes improves lysine production compared with amplification
CC of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
CC vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
CC lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
CC same strain that overexpressed lysE only produced 11.1 g/l
XX
SQ Sequence 79 BP; 21 A; 13 C; 21 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 79; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
QY 61 TATGAGCAGAGGTTTAAACA 79
DB 61 TATGAGCAGAGGTTTAAACA 79
RESULT 2
AAF26024
ID AAF26024 standard; DNA; 79 BP.
XX
AC AAF26024;
XX
DT 20-APR-2001 (first entry)
XX
DE C. glutamicum dapA MC20 mutant promoter fragment SEQ ID 5.
XX
KM lysE; L-lysine; pyc; pyruvate carboxylase; dapA; lysine exporter-carrier;
KM dihydrodipicolinate synthase; lysC; aspartate kinase; lysB; dapB;
KM dihydrodipicolinate reductase; fodder additive; ss.
XX
OS Corynebacterium glutamicum.
XX
PN EP1067193-A1.
XX
PD 10-JAN-2001.
XX
PF 06-JUL-2000; 2000EP-00114502.
XX
PR 07-JUL-1999; 99DE-01031314.
XX
PA (DEGS) DEGUSA-HUELS AG.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH.
XX
PI Kreutzner C, Moeckel B, Pfefferle W, Eggeling L, Sahn H, Patek M,
XX
PS WPI; 2001-140055/15.
XX
PT Coryneform bacteria for high level production of lysine, useful as feed
PT additive, overexpresses the pyc and at least one other gene, e.g. dapA,
PT dapB or lysE.
XX
PS Claim 4; Page 20; 28pp; German.
XX
CC This invention describes a novel L-lysine producing coryneform bacterium
CC (A) with an amplified pyc (pyruvate carboxylase) gene in which at least
CC one of the additional genes dapA (dihydrodipicolinate synthase), lysC
CC (aspartate kinase), lysB (lysine exporter-carrier) and/or dapB
CC (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
CC L-lysine is used as a fodder additive for animals. Overexpression of the
CC additional genes improves lysine production compared with amplification
CC of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
CC that overexpress dapA and all of pyc, lysE and dapB produced lysine
CC hydrochloride at 17.6 g/l after 72 hr culture at 33plusoc. The same
CC strain that overexpressed pyc only produced 11.3 g/l
XX
SQ Sequence 79 BP; 21 A; 13 C; 21 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 79; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
QY 61 TATGAGCAGAGGTTTAAACA 79
DB 61 TATGAGCAGAGGTTTAAACA 79
RESULT 3
AAF26006
ID AAF26006 standard; DNA; 79 BP.
XX
AC AAF26006;
XX
DT 20-APR-2001 (first entry)
XX
DE C. glutamicum dapA wild-type promoter DNA fragment SEQ ID 4.
XX
KM lysE; L-lysine; lysine exporter-carrier; dapA; aspartate kinase; lysC;
KM dihydrodipicolinate synthase; pyc; pyruvate carboxylase; dapB; promoter;
KM dihydrodipicolinate reductase; fodder additive; ss.
XX
OS Corynebacterium glutamicum.
XX
PN EP1067192-A1.
XX
PD 10-JAN-2001.
XX
PF 06-JUL-2000; 2000EP-00114501.
XX
PR 07-JUL-1999; 99DE-01031317.
XX
PA (DEGS) DEGUSA-HUELS AG.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Moeckel B, Pfefferle W, Kreutzner C, Hans S, Rieping M,
XX
PS Eggeling L, Sahn H, Patek M;
XX
PS WPI; 2001-125731/14.
XX
PT Coryneform bacteria for high level production of lysine, useful as feed
PT additive, overexpresses the lysE and at least one other gene,
PT particularly dapA.
XX
PS Disclosure; Page 17; 25pp; German.
XX
CC This invention describes a novel L-lysine producing coryneform bacterium
CC (A) with an amplified lysE (lysine exporter-carrier) gene in which at
CC least one of the additional genes dapA (dihydrodipicolinate synthase), lysC
CC (aspartate kinase), pyc (pyruvate carboxylase) and/or dapB
CC (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
CC L-lysine is used as a fodder additive for animals. Overexpression of the
CC additional genes improves lysine production compared with amplification
CC of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
CC vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
CC lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
CC same strain that overexpressed lysE only produced 11.1 g/l
XX
SQ Sequence 79 BP; 22 A; 13 C; 21 G; 23 T; 0 U; 0 Other;
Query Match 98.0%; Score 77.4; DB 4; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60

```

OY      61 TATGACACAGGTTTAAACA 79
DB      61 TATGACACAGGTTTAAACA 79

RESULT 4
AAAF26023
ID      AAF26023 standard; DNA; 79 BP.
XX
XX
AC      AAF26023;
XX
XX      20-APR-2001 (first entry)
DE
DE      C. glutamicum dapa wild type promoter fragment SEQ ID 4.
XX
XX      lysB; L-lysine; pyc; pyruvate carboxylase; dapa; lysine exporter-carrier;
KM      dihydrodipicolinate synthase; lysC; aspartate kinase; lysB; dapa;
KM      dihydrodipicolinate reductase; foddar additive; ss.
XX
XX      Corynebacterium glutamicum.
OS
XX      EP1067193-A1.
XX
XX      10-JAN-2001.
PD
XX
XX      06-JUL-2000; 2000EP-00114502.
PF
XX
XX      07-JUL-1999; 99DE-01031314.
PR
XX
XX      (DEGS ) DEGUSSA-HUELS AG.
PA      (KERJ ) FORSCHUNGSZENTRUM JUELICH.
PI
PI      Kreutzer C, Moeckel B, Pfefferle W, Eggeling L, Sahn H, Patek M;
DR      MPI, 2001-140055/15.
XX
XX      Coryneform bacteria for high level production of lysine, useful as feed
PT      additive, overexpresses the pyc and at least one other gene, e.g. dapa,
PT      dapa or lysE.
XX
XX      disclosure; Page 20; 28pp; German.
PS
XX
XX      This invention describes a novel L-lysine producing coryneform bacterium
CC      (A) with an amplified pyc (pyruvate carboxylase) gene in which at least
CC      one of the additional genes dapa (dihydrodipicolinate synthase) lysC
CC      (aspartate kinase), lysB (lysine exporter-carrier) and/or dapa
CC      (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
CC      L-lysine is used as a fodder additive for animals. Overexpression of the
CC      additional genes improves lysine production compared with amplification
CC      of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
CC      that overexpress dapa and all of pyc, lysB and dapa produced lysine
CC      hydrochloride at 17.6 g/l after 72 hr culture at 35pluoc. The same
CC      strain that overexpressed pyc only produced 11.3 g/l
XX
XX      Sequence 79 BP; 22 A; 13 C; 21 G; 23 T; 0 U; 0 Other;
SQ
Query Match      98.0%; Score 77.4; DB 4; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 GTTAGGTTTTTCGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB      1 GTTAGGTTTTTCGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
XX
XX
OY      61 TATGACACAGGTTTAAACA 79
DB      61 TATGACACAGGTTTAAACA 79
XX
XX
RESULT 5
AAAF71780
ID      AAF71780 standard; DNA; 1026 BP.
XX
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AC      AAF71780;
XX
XX      30-APR-2001 (first entry)
DT
XX
XX      Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:55.
DE
XX
XX      Corynebacterium glutamicum; metabolic pathway protein; MP protein;
KM      fine chemical production; microorganism; organic acid; nucleoside;
KM      nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KM      lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
KM      carbohydrate; aromatic compound; cofactor; polypeptide; enzyme; ds.
XX
XX      Corynebacterium glutamicum.
OS
XX      WO200100843-A2.
XX
XX      04-JAN-2001.
PD
XX
XX      23-JUN-2000; 2000WO-IB000923.
PF
XX
XX      25-JUN-1999; 99US-0141031P.
XX      01-JUL-1999; 99DE-01030476.
XX      02-JUL-1999; 99US-0142101P.
XX      08-JUL-1999; 99DE-01031415.
XX      08-JUL-1999; 99DE-01031418.
XX      08-JUL-1999; 99DE-01031419.
XX      08-JUL-1999; 99DE-01031420.
XX      08-JUL-1999; 99DE-01031424.
XX      08-JUL-1999; 99DE-01031428.
XX      08-JUL-1999; 99DE-01031433.
XX      08-JUL-1999; 99DE-01031435.
XX      08-JUL-1999; 99DE-01031443.
XX      08-JUL-1999; 99DE-01031453.
XX      08-JUL-1999; 99DE-01031457.
XX      08-JUL-1999; 99DE-01031465.
XX      08-JUL-1999; 99DE-01031478.
XX      08-JUL-1999; 99DE-01031510.
XX      08-JUL-1999; 99DE-01031541.
XX      08-JUL-1999; 99DE-01031573.
XX      08-JUL-1999; 99DE-01031592.
XX      08-JUL-1999; 99DE-01031632.
XX      08-JUL-1999; 99DE-01031634.
XX      08-JUL-1999; 99DE-01031636.
XX      09-JUL-1999; 99DE-01032125.
XX      09-JUL-1999; 99DE-01032126.
XX      09-JUL-1999; 99DE-01032130.
XX      09-JUL-1999; 99DE-01032186.
XX      09-JUL-1999; 99DE-01032206.
XX      09-JUL-1999; 99DE-01032227.
XX      09-JUL-1999; 99DE-01032228.
XX      09-JUL-1999; 99DE-01032229.
XX      09-JUL-1999; 99DE-01032230.
XX      14-JUL-1999; 99DE-01032922.
XX      14-JUL-1999; 99DE-01032926.
XX      14-JUL-1999; 99DE-01032928.
XX      14-JUL-1999; 99DE-01033004.
XX      14-JUL-1999; 99DE-01033005.
XX      14-JUL-1999; 99DE-01033006.
XX      12-AUG-1999; 99US-0148613P.
XX      27-AUG-1999; 99DE-01040764.
XX      27-AUG-1999; 99DE-01040765.
XX      27-AUG-1999; 99DE-01040766.
XX      27-AUG-1999; 99DE-01040832.
XX      31-AUG-1999; 99DE-01041378.
XX      31-AUG-1999; 99DE-01041379.
XX      31-AUG-1999; 99DE-01041380.
XX      31-AUG-1999; 99DE-01041394.
XX      31-AUG-1999; 99DE-01041396.
XX      03-SEP-1999; 99DE-01042076.
XX      03-SEP-1999; 99DE-01042077.
XX      03-SEP-1999; 99DE-01042079.
XX      03-SEP-1999; 99DE-01042086.
XX      03-SEP-1999; 99DE-01042087.
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PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042085.
PR 03-SEP-1999; 99DE-01042124.
PR 03-SEP-1999; 99DE-01042129.
PR 09-MAR-2000; 2000US-0187970P.
XX
PA (BAD1 ) BASF AG.
XX
PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-137957/14.
DR P-PSDB; AAB79661.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway
PT proteins, useful for producing fine chemicals in microorganisms,
PT including organic acids, nonproteinogenic amino acids, and purine and
PT pyrimidine bases.
XX
PS Claim 3; Page 235-237; 1737pp; English.
XX
CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
CC nucleic acids are useful for the production of fine chemicals in
CC microorganisms, including organic acids, nonproteinogenic amino acids,
CC purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated
CC and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
CC vitamins, cofactors, polyketides and enzymes
XX
SQ Sequence 1026 BP; 249 A; 243 C; 283 G; 251 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 4; Length 1026;
Best Local Similarity 98.7%; Pred. No. 9.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
DB 40 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 99
QY 61 TATGAGCAGAGTTTAA 79
DB 100 TATGAGCAGAGTTTAA 118
XX
RESULT 6
AAS96099
ID AAS96099 standard; DNA; 1026 BP.
XX
AC AAS96099;
XX
DT 26-FEB-2002 (first entry)
DE C. glutamicum gene #24 encoding metabolic pathway protein.
XX
XX Metabolic pathway protein; MP; lysine biosynthesis pathway;
KM methionine biosynthesis pathway; large-scale production of fine chemical;
KM Corynebacterium diptheriae; diptheria; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200166573-A2.
XX
PD 13-SEP-2001.
XX
PF 22-DEC-2000; 2000WO-IB002035.
XX
PR 09-MAR-2000; 2000US-0187970P.
PR 23-JUN-2000; 2000US-00606740.
XX
PA (BAD1 ) BASF AG.
XX
PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
PI Kim J, Lee H, Hwang B;
XX

```

```

DR WPI; 2001-582269/65.
DR P-PSDB; AAU71889.
XX
XX Nucleic acids encoding metabolic pathway proteins from Corynebacterium
PT glutamicum, useful for producing methionine and lysine in Corynebacterium
PT and Brevibacterium.
XX
PS Disclosure; Page 216-217; 316pp; English.
XX
XX The present invention relates to the isolation of novel Corynebacterium
CC glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-
CC AAU71922). The metabolic pathway proteins of the invention include
CC enzymes involved in the lysine and methionine biosynthetic pathways. The
CC polynucleotide sequences of the invention can be used for the large-scale
CC production and/or modulation of expression of fine chemicals such as
CC lysine and methionine. The sequences of the invention may be used to
CC identify C. glutamicum and related organisms e.g. C. diptheriae in a
CC subject to detect diptheria. AAS96073-AAS96132 represent C. glutamicum
CC genes encoding the novel metabolic pathway proteins of the invention
XX
SQ Sequence 1026 BP; 249 A; 243 C; 283 G; 251 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 4; Length 1026;
Best Local Similarity 98.7%; Pred. No. 9.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
DB 40 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 99
QY 61 TATGAGCAGAGTTTAA 79
DB 100 TATGAGCAGAGTTTAA 118
XX
RESULT 7
AAT84782
ID AAT84782 standard; DNA; 1411 BP.
XX
AC AAT84782;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-NOV-1997 (first entry)
XX
DE Brevibacterium lactofermentum dihydrodipicolinate synthase gene.
XX
XX Insertion sequence; transposable element; Coryneform; bacterium;
KM bacteria; amplification; artificial transposon; inverted repeat;
KM amino acid; biosynthesis; aspartokinase; dihydrodipicolinic acid;
KM synthetase; synthase; dihydrodipicolinate; ds.
XX
OS Corynebacterium glutamicum.
XX
XX Key Location/Qualifiers
FT CDS 311..1216
FT /*tag= a
FT /product= "dihydrodipicolinate_synthase"
XX
PN EP756007-A2.
XX
PD 29-JAN-1997.
XX
PF 28-JUN-1996; 96EP-00110491.
XX
PR 30-JUN-1995; 95JP-00166541.
XX
PA (AJIN ) AJINOMOTO KK.
XX
XX Moriya M, Matsui H, Yokozeki K, Hirano S, Hayakawa A, Izui M;
PI Sugimoto M;
XX
DR WPI; 1997-101858/10.

```


DR P-PSDB; AAW23283.
XX Amplifying gene, esp. aspartokinase, in Coryneform chromosome using
PT artificial transposon - useful for amino acid synthesis, esp. lysine.
XX
PS Example 5; Page 74-78; 122pp; English.
XX
CC The present sequence is a 1.5 kb chromosomal DNA region encoding the
CC Brevibacterium lactofermentum dihydrodipicolinate synthase. The fragment
CC can be used in a novel method for the amplification of a desired gene,
CC comprising the formation of an artificial transposon having a structure
CC such that a drug resistance gene and the desired gene are held between
CC inverted repeats. The artificial transposon, which is transposable in a
CC Coryneform bacterium, is transduced into a Coryneform bacterium,
CC transposed into its chromosome and the desired gene transduced and
CC amplified in the chromosome. A transposase gene is preferably held
CC between the inverted repeats, which are derived from an insertion
CC sequence of a Coryneform bacterium. The drug resistance gene is the
CC chloramphenicol or tetracycline resistance gene, and the desired gene is
CC one that participates in amino acid biosynthesis, especially an
CC aspartokinase and/or dihydrodipicolinic acid synthetase gene. (Updated on
CC 25-MAR-2003 to correct PA field.) (Updated on 17-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 309
QY 61 TATGACACAGGTTTAAACA 79
DB 310 TATGACACAGGTTTAAACA 328

RESULT 8
AAV49281 standard; DNA; 1411 BP.
XX
AC AAT49281;
XX
DT 17-OCT-2003 (revised)
DT 18-SEP-1997 (first entry)
XX
DE DNA encoding B. lactofermentum dihydrodipicolinate reductase.
XX
KM Corynebacterium, aspartokinase; feedback inhibition; L-lysine;
KM L-threonine; dihydrodipicolinate; reductase; synthase; synthetase;
KM diaminopimelate; decarboxylase; dehydrogenase; recombinant; production;
KM manufacture; fermentation; corynebacteria; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 311..1216
FT /*tag= a
FT /product= "dihydrodipicolinate_reductase"
XX
PN W09640934-A1.
XX
PD 19-DEC-1996.
XX
PF 05-JUN-1996; 96MO-JP001511.
XX
PR 07-JUN-1995; 95JP-00140614.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Otsuna S, Sugimoto M, Izui M, Hayakawa A, Nakano E, Kobayashi M;

PI Yoshihara Y, Nakamatsu T;
XX
XX WPI; 1997-052331/05.
DR P-PSDB; AAW06582.
XX
PT L-lysine production by culture of transformed Corynebacterium - using DNA
PT encoding aspartokinase lacking feedback inhibition by L-lysine, with DNA
PT coding for dihydrodipicolinate reductase.
XX
PS Example 3; Page 48-51; 90pp; Japanese.
XX
CC A novel recombinant DNA sequence functional in Corynebacterium, comprises
CC a DNA sequence encoding an aspartokinase, in which feedback inhibition by
CC L-lysine and L-threonine has been reduced, and a DNA sequence encoding
CC dihydrodipicolinate reductase and/or synthase, and/or diaminopimelate
CC decarboxylase and/or dehydrogenase, e.g. the present Brevibacterium
CC lactofermentum (ATCC 13669) dihydrodipicolinate reductase DNA sequence. A
CC Corynebacterium host transformed with the recombinant DNA sequence may be
CC used in the manufacture of L-lysine by fermentation, with an improved
CC yield and a lower fall off of production rate with culture time. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 309
QY 61 TATGACACAGGTTTAAACA 79
DB 310 TATGACACAGGTTTAAACA 328

RESULT 9
AAV40256 standard; DNA; 1411 BP.
XX
AC AAV40256;
XX
DT 17-OCT-2003 (revised)
DT 13-OCT-1998 (first entry)
XX
DE Brevibacterium lactofermentum dapA gene.
XX
KM Brevibacterium lactofermentum; lysC; L-lysine; coryneform bacterium;
KM aspartokinase; feedback inhibition; dihydrodipicolinate reductase;
KM diaminopimelate decarboxylase; aspartate aminotransferase; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 311..1213
FT /*tag= a
FT /product= "dapA"
XX
PN EP854189-A2.
XX
PD 22-JUL-1998.
XX
PF 05-DEC-1997; 97EP-00121443.
XX
PR 05-DEC-1996; 96JP-00325659.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Arai M, Sugimoto M, Yoshihara Y, Nakamatsu T;
XX
DR WPI; 1998-379060/33.
DR P-PSDB; AAW69549.

```
XX Recombinant DNA autonomously replicable in coryneform bacteria - used to
PT produce L-lysine, codes for e.g. aspartokinase, di:hydroipicolinate
PT reductase and synthase and di:amino-pimelate decarboxylase.
PS Example 3, Page 28-29; 59pp; English.
XX
CC The present invention describes a recombinant DNA autonomously replicable
CC in cells of coryneform bacteria (CB), comprising a DNA sequence coding
CC for an aspartokinase (AK) in which feedback inhibition by L-lysine and L-
CC threonine is desensitized, a DNA sequence coding for a
CC dihydrodipicolinate reductase (DHPRI), a DNA sequence coding for
CC dihydrodipicolinate synthase (DHPS), a DNA sequence coding for
CC diaminopimelate decarboxylase (DAMD) and a DNA sequence encoding dapA from
CC Brevibacterium lactofermentum. The present sequence encodes dapA from
CC Brevibacterium lactofermentum. The DNA and related products from the
CC present invention, can be used for improving L-lysine productivity by CB.
CC The L-lysine produced can be used as a fodder additive. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; Mismatches 0; Gaps 0;
Matches 78; Conservative 0; Indels 1;
QY 1 GTTAGGTTTTTTCGCGGGTTGTTAAACCCCAATGAGGAGATGTTACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGCGGGTTGTTAAACCCCAATGAGGAGATGTTACCTTGAATC 309
QY 61 TATGAGCACAGGTTTAA 79
DB 310 TATGAGCACAGGTTTAA 328
XX
RESULT 10
AAV15785
ID AAV15785 standard; DNA; 1411 BP.
XX
AC AAV15785;
XX
DT 17-OCT-2003 (revised)
DT 05-JUN-1998 (first entry)
XX
DE B. lactofermentum dihydrodipicolinate reductase DNA.
XX
KM Dihydrodipicolinate reductase; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 311..1216
FT /*tag= a
FT /product= "dihydrodipicolinate_reductase"
XX
XX EP811682-A2.
XX
XX 10-DEC-1997.
XX
XX 02-JUN-1997; 97EP-00108764.
XX
XX 05-JUN-1996; 96JP-00142812.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
PI Hitano S, Sugimoto M, Nakano E, Izui M, Hayakawa A, Yoshinara Y;
PI Nakamatsu T;
XX
XX WPI; 1998-020947/03.
DR P-PSDB; AAM47403.
XX
PT Vector containing di:amino:pimelate decarboxylase and di:amino:pimelate
PT dehydrogenase genes - used for lysine production by overexpression in
```

```
PT coryneform bacteria.
XX
PS Example 4; Page 41-43; 63pp; English.
XX
CC The present sequence encodes Brevibacterium lactofermentum
CC dihydrodipicolinate reductase. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; Mismatches 0; Gaps 0;
Matches 78; Conservative 0; Indels 1;
QY 1 GTTAGGTTTTTTCGCGGGTTGTTAAACCCCAATGAGGAGATGTTACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGCGGGTTGTTAAACCCCAATGAGGAGATGTTACCTTGAATC 309
QY 61 TATGAGCACAGGTTTAA 79
DB 310 TATGAGCACAGGTTTAA 328
XX
RESULT 11
AAH68530/C
ID AAH68530 standard; DNA; 349980 BP.
XX
AC AAH68530;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
XX
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Disclosure; SEQ ID NO 7065; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analyzing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
```

XX	Sequence	349980 BP;	86896 A;	98023 C;	80939 G;	84122 T;	0 U;	0 Other;
XX	Query Match	98.0%;	Score 77.4;	DB 5;	Length 349980;			
XX	Best Local Similarity	98.7%;	Pred. No. 5,4e-18;					
XX	Matches 78;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;			
OY	1	GTTAGCTTTTGGCGGGGTGTTTAA	CCCCCAATGAGGAAAGATGTAACCTTGAATC	60				
Db	280244	GTTAGCTTTTGGCGGGGTGTTTAA	CCCCCAATGAGGAAAGATGTAACCTTGAATC	280185				
OY	61	TATGACACAGGTTTACA	79					
Db	280184	TATGACACAGGTTTACA	280166					
RESULT 12	AAF26008	AAF26008	standard, DNA;	80 BP.				
AC	AAF26008;							
XX	20-APR-2001	(first entry)						
XX	C. glutamicum	dapA mutant MC20 promoter DNA fragment	Seq ID 6.					
XX	lysE;	L-lysine;	lysine exporter-carrier;	dapA;	aspartate kinase;	lysC;		
XX	dhidropicolinate synthase;	pyc;	pyruvate carboxylase;	dapB;	promoter;			
XX	dhidropicolinate reductase;	fodder additive;	ss.					
XX	Corynebacterium	glutamicum.						
XX	EP1067192-A1.							
XX	10-JAN-2001.							
XX	06-JUL-2000;	2000EP-00114501.						
XX	07-JUL-1999;	99DE-01031317.						
XX	(DEGS)	DEGUSSA-HUELS AG.						
XX	(KERJ)	FORSCHUNGSZENTRUM JUELICH GMBH.						
XX	Moeckel B,	Pfefferle W,	Kreutzer C,	Hans S,	Rieping M,			
XX	Eggeling L,	Sahm H,	Patek M;					
XX	WPI;	2001-125731/14.						
XX	Coryneform bacteria	for high level production of lysine,	useful as feed					
XX	additive,	overexpresses the lysE and at least one other gene,	particularly dapA.					
XX	Claim 4;	Page 18;	25pp;	German.				
XX	This invention	describes a novel L-lysine producing coryneform bacterium						
XX	(A) with an amplified	lysE (lysine exporter-carrier) gene in which at						
XX	least one of the additional	genes dapA (dihydrodipicolinate synthase), lysC						
XX	(aspartate kinase), pyc	(pyruvate carboxylase) and/or dapB						
XX	(dihydrodipicolinate reductase)	is amplified and preferably overexpressed.						
XX	L-lysine is used as a	fodder additive for animals. Overexpression of the						
XX	additional genes improves	lysine production compared with amplification						
XX	of lysE only. Corynebacterium	glutamicum DSM 5715 transformed with						
XX	vector that overexpress (i)	dapA and (ii) both lysE and dapB produced						
XX	lysine hydrochloride at	15.4 g/l after 48 hr culture at 33plusOC. The						
XX	same strain that overexpressed	lysE only produced 11.1 g/l						
XX	Sequence 80 BP;	24 A;	11 C;	21 G;	24 T;	0 U;	0 Other;	
XX	Query Match	78.0%;	Score 61.6;	DB 4;	Length 80;			
XX	Best Local Similarity	93.8%;	Pred. No. 3,8e-13;					
XX	Matches 75;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;			
OY	1	GTTAGCTTTTGGCGGGGTGTTTAA	CCCCC-AAATGAGGAAAGATGTAACCTTGAATC	59				

RESULT 13
AAAF26025
AAAF26025 standard; DNA; 80 BP.
AAAF26025
AAAF26025; (first entry)
20-APR-2001
C. glutamicum dapa MA16 mutant promoter fragment SEQ ID 6.
lysE; l-lysine; pyc; pyruvate carboxylase; dapa; lysine exporter-carrier;
dihydrodipicolinate synthase; lysC; aspartate kinase; lysE; dapB;
dihydrodipicolinate reductase; fodder additive; ss.
Corynebacterium glutamicum.
EPI067193-A1.
10-JAN-2001.
06-JUL-2000; 2000EP-00114502.
07-JUL-1999; 99DE-01031314.
(DEGS) DEGUSSA-HUELS AG.
(KERJ) FORSCHUNGSZENTRUM JUELICH.
Kreutzer C, Moeckel B, Pfeifferle W, Eggeling L, Sahm H, Patek M;
WPI; 2001-140055/15.
Coriiform bacteria for high level production of lysine, useful as feed
additive, overexpresses the pyc and at least one other gene, e.g. dapB,
dapB or lysE.
Claim 4; Page 21; 28pp; German.
This invention describes a novel l-lysine producing coryneform bacterium
(A) with an amplified pyc (pyruvate carboxylase) gene in which at least
one of the additional genes dapa (dihydrodipicolinate synthase), lysC
(aspartate kinase), lysE (lysine exporter-carrier) and/or dapB
(dihydrodipicolinate reductase) is amplified and preferably overexpressed.
l-lysine is used as a fodder additive for animals. Overexpression of the
additional genes improves lysine production compared with amplification
of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
that overexpress dapa and all of pyc, lysE and dapB produced lysine
hydrochloride at 17.6 g/l after 72 hr culture at 33plusc. The same
strain that overexpressed pyc only produced 11.3 g/l
Sequence 80 BP; 24 A; 11 C; 21 G; 24 T; 0 U; 0 Other;
Query Match 78.0%; Score 61.6; DB 4; Length 80;
Best Local Similarity 93.8%; Pred. No. 3.8e-13;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
1 GTTAGGTTTTTGGGGGTTTAAACCCCC-AAATGAGGGAAGATGTAATTGAAC 59
1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATGAGGAAGAATTAATTGAAC 60
60 CTATGACACAGGTTTAAAC 79
61 CTATGACACAGGTTTAAAC 80

```

AAH45371
ID   AAH45371 standard; DNA; 1333 BP.
XX
AC   AAH45371;
XX
DT   11-SEP-2001 (first entry)
XX
DE   C. thermoaminogenes lysin biosynthetic enzyme dapA DNA.
XX
XX   Heat-resistant; lysin biosynthesis; enzyme; coryneform;
KM   aspartate-semialdehyde dehydrogenase; dapA; ds.
XX
OS   Corynebacterium thermoaminogenes.
PN   JP2001120270-A.
XX
XX   08-MAY-2001.
XX
PF   01-NOV-1999; 99JP-00311148.
XX
PR   01-NOV-1999; 99JP-00311148.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
DR   WPI; 2001-364760/38.
XX
DR   P-PSDB; AAG64043.
XX
PT   A heat-resistant lysin biosynthetic system enzyme gene of a high
PT   temperature-resistant coryneform microbe.
XX
PS   Example 5; Page 12-13; 27pp; Japanese.
XX
CC   The invention relates to a gene from a high temperature-resistant
CC   coryneform microbe that encodes a heat-resistant lysin biosynthetic
CC   enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and
CC   can be used for growing amino acid-producing microbes. The present
CC   sequence encodes an enzyme of the invention
XX
SQ   Sequence 1333 BP; 277 A; 405 C; 397 G; 254 T; 0 U; 0 Other;
XX
Query Match          61.0%; Score 48.2; DB 4; Length 1333;
Best Local Similarity 81.2%; Pred. No. 1e-07;
Matches 56; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
QY   11 TTGCGGGGTTGTTTAAACCCCAATGAGGAGAGATGGTAACTTGAACCTATGAGACA 70
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   248 TTACGGGGTTGTGTAACCCGACCTAAGAGAGAGAGTAACTTGTGTCTCATGAGACA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY   71 GGTTTACA 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   308 GGTTTACA 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
AAF26001/c
ID   AAF26001 standard; DNA; 40 BP.
XX
AC   AAF26001;
XX
DT   20-APR-2001 (first entry)
XX
DE   C. glutamicum dapA mutant MC20 PCR primer dap2.
XX
XX   LysE; L-lysine; lysine exporter-carrier; dapA; aspartate kinase; LysC;
KM   dihydropicolinate synthase; pyc; pyruvate carboxylase; dapB; PCR primer;
KM   dihydropicolinate reductase; fodder additive; ss.
XX
OS   Corynebacterium glutamicum.
PN   EP1067192-A1.
XX
XX   EP1067192-A1.
PD   10-JAN-2001.
XX

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PF   06-JUL-2000; 2000EP-00114501.
XX
XX   07-JUL-1999; 99DE-01031317.
XX
XX   (DEGS ) DEGUSA-HUELS AG.
XX   (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI   Noeckel B, Pfeifferle W, Kreutzer C, Hans S, Rieping M;
PI   Eggeling L, Sahm H, Patek M;
XX
DR   WPI; 2001-125731/14.
XX
PT   Coryneform bacteria for high level production of lysine, useful as feed
PT   additive, overexpresses the lysE and at least one other gene,
PT   particularly dapA.
XX
XX   Example 11; Page 11; 25pp; German.
XX
CC   This invention describes a novel L-lysine producing coryneform bacterium
CC   (A) with an amplified lysE (lysine exporter-carrier) gene in which at
CC   least one of the additional genes dapA (dihydropicolinate synthase), LysC
CC   (aspartate kinase), pyc (pyruvate carboxylase) and/or dapB
CC   (dihydropicolinate reductase) is amplified and preferably overexpressed.
CC   L-lysine is used as a fodder additive for animals. Overexpression of the
CC   additional genes improves lysine production compared with amplification
CC   of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
CC   vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
CC   lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
CC   same strain that overexpressed lysE only produced 11.1 g/l
XX
SQ   Sequence 40 BP; 8 A; 10 C; 8 G; 14 T; 0 U; 0 Other;
XX
Query Match          50.6%; Score 40; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY   30 CCAATGAGGAGAGATGTAACCTGAACCTATGAGCAC 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   40 CCAATGAGGAGAGATGTAACCTGAACCTATGAGCAC 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: July 13, 2005, 17:01:40
Job time : 68.0069 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 17:00:03 ; Search time 489.728 Seconds
(without alignments)
6140.305 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 1 gctaggtttctgcgggggtt.....ctatggcacaggtttaca 79

Sequence: 1 gctaggtttctgcgggggtt.....ctatggcacaggtttaca 79

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	31.2	39.5	265	AA728069	LmLV39P7/
2	29.8	37.7	815	CR823956	GR0AA54C
3	29.8	37.7	818	CC520829	CH240.368
4	29.8	37.7	843	CR824024	GR0AA54C
5	29.8	37.7	979	BQ675212	AGENCOURT
6	28.6	36.2	439	CO670296	DC33-5812
7	28.6	36.2	624	BJ345906	BJ345906
8	28.6	36.2	665	BJ430191	BJ430191
9	28.6	36.2	674	CO588301	DG2-20b16
10	28.6	36.2	689	BU431542	BU431542
11	28.6	36.2	704	BU430317	BU430317
12	28.2	35.7	320	AU301906	AU301906
13	28.2	35.7	665	AZ640483	1M0502G03
14	28.2	35.7	1140	CC243055	CH261-84A
15	28.2	35.7	440	CO126481	GR-BD101
16	28.2	35.7	565	CB608752	AMGNUNC:N
17	28.2	35.7	663	BQ154700	NF095F071
18	28.2	35.7	889	CV266577	WS0203.B2
19	28.2	35.7	1007	CSN0073C	AL066754 Drosophila
20	27.8	35.2	472	AA664084	ac04b06.8
21	27.8	35.2	754	AI124469	SMOVL3CAN
22	27.8	35.2	784	EX183886	Danio rer
23	27.8	35.2	794	EX199920	Danio rer
24	27.6	34.9	660	BJ342553	BJ342553

25	27.6	34.9	687	9	BX214579	Danio rer
26	27.4	34.7	396	1	AV767878	AV767878
27	27.4	34.7	505	2	BE436731	BE436731
28	27.4	34.7	752	8	BZ039047	1ka22d02
29	27.2	34.4	418	7	CK105601	U233PD09
30	27.2	34.4	716	9	CL764630	OR-BBA013
31	27.2	34.4	761	5	BU301411	BU301411
32	27.2	34.4	820	5	BX467747	BX467747
33	27.2	34.4	841	5	BU525063	AGENCOURT
34	27.2	34.4	915	9	CG951244	MBEID3OTR
35	27.2	34.4	1101	9	CNS006FC	AL072117 Drosophila
36	27.2	34.4	1159	9	AG075559	Pan trogl
37	27.2	34.4	387	7	CV461820	CV461820
38	27.2	34.4	446	7	CV461809	CV461809
39	27.2	34.4	748	9	AG134983	Pan trogl
40	27.2	34.4	919	7	CK259406	EST705484
41	27.2	34.4	919	7	CK274793	CK274793
42	27.2	34.4	921	7	CK259405	EST705483
43	27.2	34.4	946	7	CK277974	EST724052
44	26.8	33.9	301	2	BB389802	BB389802
45	26.8	33.9	509	2	BF602997	BF602997

ALIGNMENTS

RESULT 1
LOCUS AA728069/c
DEFINITION LmLV39P7/129M Leishmania major promastigote full length cDNA clone
129M 5', mRNA sequence.

ACCESSION AA728069
VERSION AA728069
KEYWORDS EST.
SOURCE Leishmania major
ORGANISM Leishmania major
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

REFERENCE
1 (bases 1 to 265)
Almeida, R., Sampato, I., Schneider, H. and Blackwell, J.M.
Analysis of Leishmania major promastigote library from different stages of development
Unpublished (1998)
On Jan 5, 1998 this sequence version replaced gi:2747026.
Contact: Blackwell JM

JOURNAL
COMMENT
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hills Road,
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk
The EST is 265bp in length
PCR Primers
FORWARD: GTAAACGACGCGCCAGT
BACKWARD: GGAAACGATGACCATG
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 265.
Location/Qualifiers
1..265
/organism="Leishmania major"
/mol_type="mRNA"
/strain="LV39"
/db_xref="taxon:5664"
/clone="129M"
/cell_type="Promastigote"
/clone_id="Leishmania major promastigote full length cDNA library from logarithmic stage (day 7)"
/note="Vector: Lambda Zap II; Site_1: XhoI; Site_2: NotI"

FEATURES

ORIGIN

Query Match 39.5%; Score 31.2; DB 1; Length 265;
Best Local Similarity 66.2%; Pred. No. 5.4;

Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 4 AGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTAACCTGTAATCTAT 63
 Db 152 AGGCTTTTGGGGGTTGTAATCGCCCAAGAGCTCGGCAAGTGCATTAACAGCTCC 93

Qy 64 GAGCAGCAG 71
 Db 92 CAGCAGCAG 85

RESULT 2

CR823956/c

LOCUS CR823956 815 bp DNA linear GSS 27-SEP-2004
 DEFINITION GR00AA54CB05F01 INRA BAC Bos taurus genomic clone INRA_984E06, DNA

ACCESSION CR823956
 VERSION CR823956.1 GI:52760044

KEYWORDS GSS.
 SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos

REFERENCE 1 (bases 1 to 815)

AUTHORS Eggen,A., Schibler,L. and Roy,A.

JOURNAL Bovine BAC End Sequences from the INRA bovine BAC library

REFERENCE 2 (bases 1 to 815)

AUTHORS Genoscope.

JOURNAL Direct Submission

COMMENT Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr)

CONTACT : Andre Eggen

DEPARTMENT : Animal Genetics - LGBC

INRA

78350 Jouy-en-Josas, France

Tel: 33 1 34 65 24 24

Fax: 33 1 34 65 24 78

Email: eggen@jouy.inra.fr

Clones are derived from the INRA bovine BAC library
 (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library

availability, please contact Andre Eggen (eggen@jouy.inra.fr). This

work was undertaken as part of the International Bovine BAC

Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope

(Evry) Plate: 984 row: E column: 06

Seq primer: M13 Forward

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..815

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Holstein"

/db_xref="taxon:9913"

/clone="INRA_984E06"

/sex="Male"

/cell_type="fibroblast"

/clone_lib="INRA bovine BAC"

/note="Vector: pBelobAC11, Site_1: HindIII, Holstein bull;"

INRA Bovine BAC library (Male) produced by Andre

Eggen-genoscope sequence ID : GR00AA54CB05F01"

ORIGIN

Query Match 37.7%; Score 29.8; DB 9; Length 815;

Best Local Similarity 75.5%; Pred. No. 20;

Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTA 50

Db 728 TCAAGGTTTTCGGGGGTTTTCCTCTCTAAGGAGGAGATGCTTA 680

RESULT 3

CC520829/c

LOCUS CC520829 818 bp DNA linear GSS 17-JUN-2003
 DEFINITION CH240_36814.T7 CHORI-240 Bos taurus genomic clone CH240_36814,

ACCESSION CC520829
 VERSION CC520829.1 GI:31839117

KEYWORDS GSS.
 SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos

REFERENCE 1 (bases 1 to 818)

AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,

Tsai,M., Cloutier,A., Lee,D., Gilm,N., Olson,T., Mayo,M.,

Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,

Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,

Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,

Dalrymple,B.P. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

Unpublished (2003)

Other GSSs: CH240_36814.TARBA13P2

Contact: Rob Holt

Sequencing The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering/information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 368 row: I column: 4

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..818

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Hereford"

/db_xref="taxon:9913"

/clone="CH240_36814"

/sex="Male"

/cell_type="Blood"

/clone_lib="CHORI-240"

/note="Vector: pTARBAC1.3, Site_1: MboI, Site_2: MboI;

Hereford bull in Domino 9937; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 37.7%; Score 29.8; DB 9; Length 818;

Best Local Similarity 75.5%; Pred. No. 20;

Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTA 50

Db 314 TCAAGGTTTTCGGGGGTTTTCCTCTCTAAGGAGGAGATGCTTA 266

RESULT 4

CR824024/c

LOCUS CR824024 843 bp DNA linear GSS 27-SEP-2004
 DEFINITION GR00AA54CE07F01 INRA BAC Bos taurus genomic clone INRA_982H08, DNA

ACCESSION CR824024
 VERSION CR824024.1 GI:52760112

KEYWORDS GSS.

SOURCE
ORGANISM Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 843)
REFERENCE Eggen, A., Schibler, L. and Roy, A.
TITLE Bovine BAC End Sequences from the INRA bovine BAC library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 843)
GENOSCOPE Genoscope.
DIRECT SUBMISSION Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
URL Web : www.genoscope.cns.fr
CONTACT Andre Eggen
DEPARTMENT Department of Animal Genetics - LGBC
INRA INRA
 78350 Jouy-en-Josas, France
 Tel : 33 1 34 65 24 24
 Fax : 33 1 34 65 24 78
 Email : eggen@jouy.inra.fr
 Clones are derived from the INRA bovine BAC library (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library availability, please contact Andre Eggen (eggen@jouy.inra.fr). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope (Evry) Place: 982 row: H column: 08
 Seq primer: M13 Forward
 Class: BAC ends.
LOCATION/QUALIFIERS
 1..843
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Breed: Holstein"
 /db_xref="taxon:9913"
 /clone="INRA_982H08"
 /sex="Male"
 /cell_type="fibroblast"
 /clone_lib="INRA bovine BAC"
 /note="Vector: pBelBAC11; Site 1: HindIII; Holstein bull; INRA Bovine BAC library (Male) produced by Andre Eggen-Genoscope sequence ID : GR0AAS4CE07FM1"

ORIGIN
 Query Match 37.7%; Score 29.8; DB 9; Length 843;
 Best Local Similarity 75.5%; Pred. No. 20;
 Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGATA 50
 Db 729 TCAGGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGGTTAA 681

RESULT 5
LOCUS B0675212 979 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8355129 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275416
ACCESSION B0675212
VERSION B0675212.1 GI:21786046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 979)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph. D.
COMMENT Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

FEATURES
source
 1..979
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6275416"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 36.7%; Score 29; DB 5; Length 979;
 Best Local Similarity 67.2%; Pred. No. 39;
 Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGATACTTGAACCT 61
 Db 780 TTGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGGTTAAACGCC 839

QY 62 A 62
 Db 840 A 840

RESULT 6
LOCUS CO670296/c 499 bp mRNA linear EST 26-JUL-2004
DEFINITION DG33-5832 DG33-aorta Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO670296
VERSION CO670296.1 GI:50613981
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 499)
REFERENCE Schluter, T., Hermanns, J., Weindel, M., Schutte, D., Kranz, H.,
 Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
CONTACT Thomas Schluter
COMMENT LION Bioscience AG
 Waldoferstrasse 98, D-69123 Heidelberg, Germany
 Tel: +49 6221 4038 150
 Fax: +49 6221 4038 290
 Email: Thomas.Schluter@lionbioscience.com.
LOCATION/QUALIFIERS
 1..499
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="aorta"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="DG33-aorta"

ORIGIN /note="Organ: aorta; Vector: Dog pBluescript LION"

Query Match 36.2%; Score 28.6; DB 7; Length 499;
Best Local Similarity 64.2%; Pred. No. 48;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 13 GCGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGACTCTATGACACAG 72
Db 489 GTGGGTTTCGTTGAGCTTAAATGAGGAGTACATGTTGTGAATCTTTGCTATCAT 430

Qy 73 TTAAACA 79
Db 429 GTTAAACA 423

RESULT 7
Bj345906 624 bp mRNA linear EST 06-MAR-2002
LOCUS Bj345906 Dictyostelium discoideum cDNA library, AF Dictyostelium
DEFINITION Bj345906 Dictyostelium cDNA clone dd429p09 3', mRNA sequence.
ACCESSION Bj345906
VERSION Bj345906.1 GI:19216413
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE 1 (bases 1 to 624)
AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE Full length cDNA of Dictyostelium discoideum at the aggregation stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
source 1..624
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dd429p09"
/sex="mat A"
/dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"

ORIGIN

Query Match 36.2%; Score 28.6; DB 4; Length 624;
Best Local Similarity 72.5%; Pred. No. 49;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTTTAACCCCAATGAGGAGAGTGAACCTTGACTCTATGACGA 68
Db 530 GTGGTTAAATCAACCAATGATGATATGGAACCATGATACCTTTAGCA 580

RESULT 8
Bj430191 665 bp mRNA linear EST 13-MAR-2002
LOCUS Bj430191 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION Bj430191 Dictyostelium cDNA clone ddv6108 3', mRNA sequence.
ACCESSION Bj430191
VERSION Bj430191.1 GI:19404913
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE 1 (bases 1 to 665)
AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

TITLE Full length cDNA of Dictyostelium discoideum at the vegetative stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
source 1..665
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv6108"
/sex="mat A"
/dev_stage="Growth phase"
/clone_lib="Dictyostelium discoideum cDNA library, VF"

ORIGIN

Query Match 36.2%; Score 28.6; DB 4; Length 665;
Best Local Similarity 72.5%; Pred. No. 50;
Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTTTAACCCCAATGAGGAGAGTGAACCTTGACTCTATGACGA 68
Db 571 GTGGTTAAATCAACCAATGATGATATGGAACCATGATACCTTTAGCA 621

RESULT 9
CO588301 674 bp mRNA linear EST 21-JUL-2004
LOCUS CO588301 DG2-20b16 Dog brain Canis familiaris cDNA 3', mRNA sequence.
DEFINITION CO588301
ACCESSION CO588301
VERSION CO588301.1 GI:50433822
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 674)
AUTHORS Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H., Heinrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schueter@lionbioscience.com.
Location/Qualifiers
FEATURES
source 1..674
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG2-brain"
/note="Organ: brain; Vector: Dog pBluescript LION"

ORIGIN

Query Match 36.2%; Score 28.6; DB 7; Length 674;
Best Local Similarity 64.2%; Pred. No. 50;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 13 GCGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGACTCTATGACACAG 72
Db 486 GTGGGTTTCGTTGAGCTTAAATGAGGAGTACATGTTGTGAATCTTTGCTATCAT 427

Qy 73 TTAAACA 79
 |||||
 Db 426 GTTAACA 420

RESULT 10
 BJ431542 689 bp mRNA linear EST 13-MAR-2002
 LOCUS BJ431542
 DEFINITION dictyostelium discoideum cDNA library, VF Dictyostelium
 accession cDNA clone d4v14416 3', mRNA sequence.

ACCESSION BJ431542
 VERSION BJ431542.1 GI:19406264
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
 1 (bases 1 to 689)
 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
 Full length cDNA of Dictyostelium discoideum at the vegetative
 stage

JOURNAL
 COMMENT Unpublished (2002)
 Contact: Tadao Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers

FEATURES
 source
 1. 689
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="ddv1416"
 /sex="mat A"
 /dev_stage="Growth phase"
 /clone_1fb="Dictyostelium discoideum cDNA library, VF"

ORIGIN
 Query Match 36.2%; Score 28.6; DB 4; Length 689;
 Best Local Similarity 72.5%; Pred. No. 50;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTGTTTAAACCCCAATGAGGAGATGTAACCTTGAACTATAGACA 68
 |||||
 Db 497 GTGTTTAAATCACCACCAATGCATGATATGGAACCATGACACTTTTACCA 547

RESULT 11
 BJ430317 704 bp mRNA linear EST 13-MAR-2002
 LOCUS BJ430317
 DEFINITION dictyostelium discoideum cDNA library, VF Dictyostelium
 accession cDNA clone d4v6g22 3', mRNA sequence.

ACCESSION BJ430317
 VERSION BJ430317.1 GI:19405039
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
 1 (bases 1 to 704)
 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
 Full length cDNA of Dictyostelium discoideum at the vegetative
 stage

JOURNAL
 COMMENT Unpublished (2002)
 Contact: Tadao Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source
 1. 704
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="d4v6g22"
 /sex="mat A"
 /dev_stage="Growth phase"
 /clone_1fb="Dictyostelium discoideum cDNA library, VF"

ORIGIN
 Query Match 36.2%; Score 28.6; DB 4; Length 704;
 Best Local Similarity 72.5%; Pred. No. 50;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTAAACCCCAATGAGGAGATGTAACCTTGAACTATAGACA 68
 |||||
 Db 536 GTGTTTAAATCACCACCAATGCATGATATGGAACCATGACACTTTTACCA 586

RESULT 12
 AU301906 320 bp mRNA linear EST 22-JUN-2004
 LOCUS AU301906
 DEFINITION elegans cDNA clone Z10294, mRNA sequence.

ACCESSION AU301906
 VERSION AU301906.1 GI:41117765
 KEYWORDS EST.
 SOURCE Zinnia elegans
 ORGANISM Zinnia elegans
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Zinnia.
 1 (bases 1 to 320)
 Demura,T., Taohiro,G., Horiguchi,G., Kishimoto,N., Kubo,M.,
 Matsumoto,N., Minami,A., Nagata-Hiwatashi,M., Nakamura,K.,
 Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
 Fukuda,H.
 Visualization by comprehensive microarray analysis of gene
 expression programs during transdifferentiation of mesophyll cells
 into xylem cells
 Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)

JOURNAL
 COMMENT Morphogenesis Research Group
 RIKEN Plant Science Center
 1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9605
 Fax: 81-45-503-9573
 Email: demura@postman.riken.go.jp
 This clone was obtained at our laboratory
 Seq primer: M13 forward.
 Location/Qualifiers

FEATURES
 source
 1. 320
 /organism="Zinnia elegans"
 /mol_type="mRNA"
 /cultivar="canary bird"
 /db_xref="taxon:34245"
 /clone="Z10294"
 /library="mesophyll cell"
 /clone_1fb="zinnia cultured mesophyll cell equalized cDNA"
 /note="Vector: pGEM-T easy; cultured in tracheary element
 differentiation-inductive medium"

ORIGIN
 Query Match 35.7%; Score 28.2; DB 1; Length 320;
 Best Local Similarity 68.4%; Pred. No. 61;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTTTGGGGGTTGTTTAAACCCCAATGAGGAGATGTAACCTTGAAAC 58
 |||||
 Db 193 TTCAATTTGCTTCGGGTTTGGTTAAATCCAAACGAGCAATATGCAATATTAGAC 249

RESULT 13
 AZ640483/c 665 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0502G03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 DEFINITION clone UUGCIM0502G03 R, genomic survey sequence.
 ACCESSION AZ640483
 VERSION AZ640483.1 GI:11763883
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 665)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weise, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std. Error: 0.00
 Plate: 0502 row, G column: 03
 Seg primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 665.
 Location/Qualifiers
 1. 665
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0502G03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 35.7%; Score 28.2; DB 8; Length 665;
 Best Local Similarity 68.4%; Pred. No. 69;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 2 TTAGGTTTGGGGGTTGTTTAAACCCCAATGAGGAGATGTACTTGAAC 58
 Db 393 TTAGTACTTTCCATATTTTCAAGCAGATGAGGCCAGATTGTACATTAAAC 337

RESULT 14
 CC243055/c 1140 bp DNA linear GSS 12-MAY-2003
 LOCUS CH261-84A2 RML.1 CH261 Gallus gallus genomic clone CH261-84A2,
 DEFINITION genomic survey sequence.
 ACCESSION CC243055
 VERSION CC243055.1 GI:30569718
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1140)
 Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 JOURNAL Unpublished (2003)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.edu
 Insert length: 18200 Std. Error: 0.00
 Seg primer: RML TACGACTCCTATAGGAGCA
 Class: BAC ends
 High quality sequence start: 34
 High quality sequence stop: 581.
 Location/Qualifiers
 1. 1140
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-84A2"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: PTARBAC2.1, site_1: EcoRI, site_2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.choi.org/bacpac"

ORIGIN
 Query Match 35.7%; Score 28.2; DB 8; Length 1140;
 Best Local Similarity 63.6%; Pred. No. 75;
 Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 5 GGTTTTGGGGGCTGTTTAAACCCCAATGAGGAGATGTACTTGAAC 64
 Db 1047 GGTTTTGGGGGCTTATTTCCTCCCTCCCACTGAGTGAATCTTCAAGAGGTG 988

RESULT 15
 CO126481 440 bp mRNA linear EST 16-JUN-2004
 LOCUS GR_Eb10112 r GR_Eb Gossypium raimondii cDNA clone GR_Eb10112 3',
 DEFINITION mRNA sequence.
 ACCESSION CO126481
 VERSION CO126481
 KEYWORDS EST.
 SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 1 (bases 1 to 440)
 Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
 Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and

TITLE Wing, R.A.
Global assembly of Cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: <http://genome.arizona.edu>
Plate: 10 row: I column: 12.

FEATURES
Source Location/Qualifiers
1. .440
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Bh10112"
/issue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_Eb"
/note="Vector: pCMV SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; library made by invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by Agt. More glycerol clones held in -80."

ORIGIN

Query Match 35.4%; Score 28; DB 7; Length 440;
Best Local Similarity 63.2%; Pred. No. 75;
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Q5	GGTTTTCGGGGGTTTAAACCCCAATGAGGAGAGATGTAACCTTGAACCTATG	64
Db	250 GGATTTAACTTAATTTTCCGCCCAAGCGGGGAGAGAGTTTGCATGACACATG	191
QY	65 AGCACAGG	72
Db	190 TGCCCAAG	183

Search completed: July 13, 2005, 19:41:20
Job time : 497.728 secs

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